

GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Om nucleic - nucleic search, using BW model

Run on: May 24, 2004, 23:42:47 ; Search time 2250 Seconds
(without alignments)
10267.483 Million cell updates/sec

Title: US-10-623-891-2

Perfect score: 533

Sequence: 1 tgtggggggggctccgggg.....cgtagtatttcggtaacaca 533

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenBank:

- 1: gb_bai:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_sts:*
- 7: gb_Ph:*
- 8: gb_p1:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sv:*
- 12: gb_tat:*
- 13: gb_un:*
- 14: gb_v1:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_on:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sb:*
- 28: em_v1:*
- 29: em_vn:*
- 30: em_hgt_hum:*
- 31: em_hgt_inv:*
- 32: em_hgt_other:*
- 33: em_hgt_mus:*
- 34: em_hgt_pln:*
- 35: em_hgt_rod:*
- 36: em_hgt_mam:*
- 37: em_hgt_vrt:*
- 38: em_hgt_vrt:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

RESULT 1

Result No.	Score	Query Match	Length	DB	ID	Description	
1	C=533—100-0—	585	14	SB2226		S82226 {RS region, M2223 Reticuloendo	
2	507.8	95.3	1005	1A	ACBLTR1	AP006055 Folipox v	
3	506	94.9	4292	1A	AF006055	AF246598 Folipox v	
4	506	94.9	8221	1A	AF246598	M2224 Reticuloendo	
5	503	94.4	827	1A	ACBLTR2	AY255632 Folipox v	
6	490.8	92.1	745	1A	AY255632	A83548 Sequence 1	
7	439.4	82.4	940	6	BD006232	BD00622 Novel int	
8	439.4	82.4	6			ST79845 {LTR_U3' R	
9	438.4	82.3	545	1A	S79845	VOL205 Spleen necr	
10	429	80.5	583	1A	REV	VOL1204 Spleen necr	
11	313.8	58.9	859	14	REXX2	AF006066 Folipox v	
12	313.8	58.9	891	14	REXX1	AY255633 Folipox v	
13	206.4	38.7	1022	1A	AF006066	AF006064 Folipox v	
14	193	36.2	485	1A	AV255633	AF006064 Folipox v	
15	193	36.2	2640	1A	AF006064	AF006064 Folipox v	
16	193	36.2	288539	1A	AF198100	AF198100 Folipox v	
17	155	29.1	578	6	A83549	A83549 Sequence 2	
18	155	29.1	578	6	BD006233	BD006233 Novel int	
19	130.4	24.5	1530	14	RESNVX	VOL1200 Spleen necr	
20.	119.6	22.4	160	5	CHKSINV12	M1220 Spleen necr	
21.	119.6	22.4	160	5	CHKSINV12	M12242 Spleen necr	
22.	119.6	22.4	160	5	CHKSINV12	M12244 Spleen necr	
23.	119.6	22.4	160	5	CHKSINV12	M1224 Spleen necr	
24.	119.6	22.4	160	5	CHKSINV12	M12248 Chicken DNA	
25.	119.6	22.4	160	5	CHKSINV12	M12250 Spleen necr	
26.	105.2	19.9	180	14	SNVLT	X5950 Spleen necr	
27.	80.8	15.2	163	14	SNVPRTRB	M12297 Spleen necr	
28.	64.8	12.2	100	14	SNVLT12	M19315 Spleen necr	
29.	58.4	11.0	209	14	SNVPTRDA	M12208 Spleen necr	
30.	44.8	8.4	69	5	CHKSINV12	M12241 Chicken DNA	
31.	42.6	8.0	63	5	CHKSINV12	M12249 Chicken DNA	
32.	42.6	8.0	69	5	CHKSINV12	M12205 Chicken DNA	
33.	42.6	8.0	69	5	CHKSINV12	M12245 Chicken DNA	
34.	7.9	69	5		CHGSINV12	M12243 Chicken DNA	
35.	42.2	7.9	69	5	CHGSINV12	M12247 Chicken DNA	
36.	40.4	7.6	100	14	SNVLT12	M19314 Spleen necr	
c	37.	7.4	15583	5	AL935041	AL935041 Zebrafish	
c	38.	7.4	167563	5	AL92888	AL92888 Zebrafish	
c	39.	7.4	182325	5	BX004869	BX004869 Zebrafish	
c	40.	7.4	186924	2	BX005365	BX005365 Danio rer	
c	41.	39.6	7.4	207161	2	BX530067	BX530067 Danio rer
c	42.	39.6	7.4	211383	2	BX119319	BX119319 Danio rer
c	43.	39.6	7.4	219981	2	BX544872	BX544872 Danio rer
c	44.	39.6	7.4	224806	2	BX004858	BX004858 Danio rer
c	45.	39.2	7.4	237323	10	AL772376	AL772376 Mouse DNA

ALIGNMENTS

RESULT 1

LOCUS	DEFINITION	585 bp	DNA	linear	VRL 12-FEB-1997
S82226	{RS region, intervening sequence}		[Marek's disease virus MDV, RML, Gallid herpesvirus 2]		
DEFINITION	Genomic DNA, 585 nt.				
ACCESSION	S82226				
VERSION	S82226.1				
KEYWORDS					
SOURCE	Gallid herpesvirus 2				
ORGANISM	Gallid herpesvirus 2				
REFERENCE	Viruses; dsDNA viruses; no RNA stage; Herpesviridae; Alphaherpesvirinae; Marek's disease-like viruses.				
AUTHORS	J.Wones,D.,Brunovskis,P.,Witter,R.,and Kung,H.-J.,				
TITLE	Retroviral insertion activation in a herpesvirus transcriptional				

Pred. No. is the number of results predicted by chance to have a

Query Match		94.9%	Score	505	DB	14	Length	4292;		
Best Local Similarity		100.0%	Pred.	No.	1-1e-14		Matches			
Matches		50;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	28	GGAGGGAGCTCCGGGGGATAGGGCTGCTCGTAACGCCATTAGTCCTGTAATC	87							
Db	908	GGAGGGAGCTCCGGGGGATAGGGCTGCTCGTAACGCCATTAGTCCTGTAATC	967							
Qy	88	ATSCCTTGCTGCCTTAAGCCCATTTGACTGTGATAATTTCGCTGATATTCCTCGGA	147							
Db	968	ATGCTTGCTTGCTTAGCCGCAATTGACTGTGATAATTTCGCTGATATTCCTCGGA	1027							
Qy	148	ATCCGATCAGAGCGGCTCATAACTAAGCTTAAGGAATGTTGTTGAGGAGACATC	207							
Db	1028	ATCCGATCAGAGCGGCTCATAACTAAGCTTAAGGAATGTTGTTGAGGAGACATC	1087							
Qy	208	AGACCACTTGACCATCCATCAGAACACAGGAGTCGAACTATCACTGAGCAA	267							
Db	1088	AGACCACTTGACCATCCATCAGAACACAGGAGTCGAACTATCACTGAGCAA	1147							
Qy	268	TGATGTGAAAGGCGAGTCGCTTCTCCATGAGGAAATGTCATGCAACATCTGTAA	327							
Db	1148	TGGTGTGAAAGGCGAGTCGCTTCTCCATGAGGAAATGTCATGCAACATCTGTAA	1207							
Qy	328	GCAGCTTAACTAGCGGGCATCTCTCTCGGGTCCATCACATGTTGCA	387							
Db	1208	GCAGCTTAACTAGCGGGCATCTCTCTCGGGTCCATCACATGTTGCA	1267							
Qy	388	CCTCGGCCAGATCGATACTGAACTAAAGCTTTCTCTCTATCCCTGAGATGGCA	447							
Db	1268	CCTCGGCCAGATCGATACTGAACTAAAGCTTTCTCTCTATCCCTGAGATGGCA	1327							
Qy	448	GTGAGGAGATTTCGCTGGCTGCTGGTACGGGGGGTAGGATCCGGAC	507							
Db	1328	GTGAGGAGATTTCGCTGGCTGCTGGTACGGGGTAGGATCCGGAC	1387							
Qy	508	TGAATCCGAGTATTCTGGTACACA	533							
Db	1388	TGAATCCGAGTATTCTGGTACACA	1413							
RESULT 4										
LOCUS	AF246698	AF246698	8221	bp	DNA	linear	VRL	12-MAR-2003		
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
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AUTHORS										
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REMARK Sequence update by submitter
On Mar 12, 2003 this sequence version replaced gi:8926141.
LOCATIONS
source

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University of Illinois field strain; integrated provirus"
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LTR
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ORIGIN

	Query	Match	94.9%	Score	506;	DB	14;	Length	8221;	
	Best	Local	Similarity	10.0%	; Pred.	No.	1	2e-14;		
	Matches	506;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
Qy	28	GGAGGGAGCTCGGGGGATAGGCCCTGGCTCCTAACCTGCCTATTAGCTCTGTGATC	87							
Db	68	GGAGGAGACTCCGGGCGATAGGCCCTGGCTCCTAACCTGCCTATTAGCTCTGTGATC	127							
Qy	88	ATGCTGCTGCTGCTTAGGCCCATGTTACTTGATATATTCCGTGATATCATTCCTCGGA	147							
Db	128	ATGCTGCTGCTGCTAGGCCATGTTACTTGATATATTCCGTGATATCATTCCTCGGA	187							
Qy	148	ATGGCACTCAAGAGCAGGCTCTAAACATATAAGGAATGTTGTTGAAGGCAACATC	207							
Db	188	ATGGCACTCAAGAGCAGGCTCTAAACATATAAGGAATGTTGTTGAAGGCAACATC	247							
Qy	208	AGACCACTTGACCATCACTCACGACAACACGAGATGAGACTATCATCTGAGCA	267							
Db	248	AGACCACTTGACCATCACTCACGACAACACGAGATGAGACTATCATCTGAGCA	307							
Qy	268	TGTTGTGAAAGGGCAGATGCTCTCCATAGGSSAAATGTCGCAACATCCCTGAA	327							
Db	308	TGTTGTGAAAGGGCAGATGCTCTCCATCCATGAGGAAATGTCGCAACATCCCTGAA	367							
Qy	328	GGGGTATATAGCCAGGTGATCTCTGCTGGGGTGGCTCTAACATGTTGTTGA	387							
Db	368	GGGGTATATAGCCAGGTGATCTCTGCTGGGGTGGCTCTAACATGTTGTTGA	427							
Qy	388	CCTGGCGCCGAGATGGAATCTGTTGATAAAAGCTTTCTCTATATCTCAGATGGCA	447							
Db	428	CCTGGCGCCGAGATGGAATCTGTTGATAAAAGCTTTCTCTATATCTCAGATGGCA	487							
Qy	448	GTGAGAGGAGATTTCGCGGTTGGCTGGCTACTGGTGGCTGGCTGGCTGGAC	507							
Db	488	GTGAGAGGAGATTTCGCGGTTGGCTGGCTACTGGTGGCTGGCTGGAC	547							
Qy	508	TGAATCGCTGATTCGGTACACA	533							
Db	548	TGAATCGCTGATTCGGTACACA	573							

RESULT 5
ACRLTR2
ACRLTR2
DEFINITION Reticuloendotheliosis virus 887 bp ss-RNA linear VRL 27-APR-1993
LOCUS 887
DEFINITION Reticuloendotheliosis virus 713 proviral clone RNA.
ACCESSION M2224
VERSION M2224_1
KEYWORDS GI:20709
SOURCE long terminal repeat (LTR)
ORGANISM Reticuloendotheliosis virus
Viruses: Retroviridae: Gamma-retroviridae

Qy	268	TGGTGTAAAGGCAAGATGTTATCCCTCAAATGACGGAAATGTCATGCACATCTGTA	327	Qy	358	TGGGGTCCCGCTTACACATGTCACGTGCGGCCAGATTCGATCTGTAATAA	417
Db	308	TGGTGTAAAGGCAAGATGTTATCCCTCAAATGACGGAAATGTCATGCACATCTGTA	367	Db	361	TGGGGTCCCGCTTACACATGTCACGTGCGGCCAGATTCGATCTGTAATAA	420
Qy	328	GCGGCTATATAAGCCAGGTCATCTCTGCTCGGGTCCGCTACATGCAATCTGAA	387	Qy	418	AG-CTTTCTCTATCCTCAGATGGCAGTGAGGAGATTGTCCTGGGTGTTG	476
Db	368	GCGGCTATATAAGCCAGGTCATCTCTGCTCGGGTCCGCTACATGCAATCTGAA	427	Db	421	AGTGTTCCTCTATACCTCAGATGGCAGTGAGGAGATTGTCCTGGGTGTTG	480
Qy	388	CGTGGGCCAGATGGAATCTGTAATAAGCTTCTCTATATCTCAGATGTCGA	447	Qy	477	CTGACCTACTGGGGTAGGGATCCGACTGAACTGCTGTTATTCGATGAAACA	533
Db	428	CTGCGGCCAGATGGAATCTGTAATAAGCTTCTCTATATCTCAGATGTCGA	487	Db	481	CTGGCTACTGGGGTAGGGATCCGACTGAACTGCTGTTATTCGATGAAACA	537
Qy	448	GTGAGGAGATTGTTGCTGGCTACTGGGGTAGGGATCCGACTGAACTGCTGGA	507				
Db	488	GTGAGGAGATTGTTGCTGGCTACTGGGGTAGGGATCCGACTGAACTGCTGGA	547				
Qy	508	TGATCCCTGATTCGGTACACA	533				
Db	548	TGAAT-CGTCGTAGTCGGTACACA	572				
RESULT 7							
LOCUS	A83548			DEFINITION	A83548		
DEFINITION	Sequence 1 from Patent WO9849334.	940 bp	DNA	LINEAR	PAT 21-JAN-2000		
ACCESSION	A83548			VERSION	A83548		
KEYWORDS				ACCESSION	BD006232		
SOURCE				VERSION	BD006232		
ORGANISM				KWONDS	JP 200150021-A1		
REFERENCE				COMMENT			
AUTHORS	1 Gallo, C. and Darlix, J.			REFERENCE	Viruses; Retroviridae; Gammaretrovirus.		
TITLE	NOVEL INTERNAL RIBOSOME ENTRY SITE AND VECTOR CONTAINING SAME			AUTHORS	Lasra, M.L., Darlix, C.G. and Darlix, J.L.		
JOURNAL	PATENT: WO 9849334-A 1 NOV-1998;			JOURNAL	Novel internal ribosome entry site and vector containing same		
FEATURES	GABUS DARLIX CAROLINE (FR); INST NAT SANTE RECH MED (FR)			PATENT	JP 200150021-A 09-JAN-2001;		
source	Location/Qualifiers			INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE			
	1. .940			COMMENT	Reticuloendotheliosis virus		
	/mol_type="unassigned DNA"			ORGANISM	Reticuloendotheliosis virus		
	/strain="TYPE A (REV-A)"			COMMENT	Viruses; Retroviridae; Gammaretrovirus.		
	/isolate="LEADER 5' DE L'ARN GENOMIQUE REV-A"			REFERENCE	1 (bases 1 to 940)		
	/db_xref="taxon:11636"			AUTHORS	1 to 940		
ORIGIN				JOURNAL	Lasra, M.L., Darlix, C.G. and Darlix, J.L.		
Query Match	82.4%; Score 439.4; DB 6; Length 940;			PATENT	Patent: JP 200150021-A 09-JAN-2001;		
Best Local Similarity	93.3%; Pred. No. 3.8e-14;			INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE			
Matches	501; Conservative 0; Mismatches 11; Indels 25; Gaps 3;			COMMENT	Reticuloendotheliosis virus		
Qy	22	ATGGGGAGGACTCCGGGGAATAGCGCTACTGCATTTAGCTCT	81	ORGANISM	Reticuloendotheliosis virus		
Db	1	ATGGGGAGGACTCCGGGGAATAGCGCTACTGCATTTAGCTCT	60	COMMENT	Viruses; Retroviridae; Gammaretrovirus.		
Qy	82	GTAATCATGCTCTCTGCTTGCCTGGCGCATCTACTGATTTAGCTGAT-----	134	REFERENCE	1 (bases 1 to 940)		
Db	61	GTAATCATGCTCTGCTTGCCTTGCCTGGCGCATCTACTGATTTAGCTGAT-----	120	AUTHORS	1 to 940		
Qy	135	-----ATCATTCGGAAATGGGATCAAGAGCAGCTCATAAACCTAAAG	182	JOURNAL	Novel internal ribosome entry site and vector containing same		
Db	121	CTGGGAATGGGATCAATTCGGAAATGGGATCAAGAGCAGCTCATAAAG	180	PATENT	JP 200150021-A 09-JAN-2001;		
Qy	183	GAATGTTGTTGAAAGGCAAGATCAGACCTTCATCAACACAG	242	INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE			
Db	181	GAATGTTGTTGAAAGGCAAGATCAGACCTTCATCAACACAG	240	COMMENT	Reticuloendotheliosis virus		
Qy	243	AGATCGACTTATCATCTGACCGAATGGTGAAGGGAGATCTATCTCATGAG	302	ORGANISM	Reticuloendotheliosis virus		
Db	241	AGATCGACTTATCATCTGACCGAATGGTGAAGGGAGATCTATCTCATGAG	302	COMMENT	Viruses; Retroviridae; Gammaretrovirus.		
Qy	303	GAATGTTGCTCATGCAACATCTCTGTCCTGTAAGGGCTTATACCGAGGTG	357	AUTHORS	1 to 940		
Db	301	GAATGTTGCTCATGCAACATCTCTGTCCTGTAAGGGCTTATACCGAGGTG	360	JOURNAL	Novel internal ribosome entry site and vector containing same		
Qy	303	GAATGTTGCTCATGCAACATCTCTGTCCTGTAAGGGCTTATACCGAGGTG	357	PATENT	JP 200150021-A 09-JAN-2001;		

Db 301 GAGATGTCATGCACATCCTGTCCTGTAGCGCTATAACCAGGTGCTCTG 360
 Qy 358 TCGGGTCCGCTCTACATGTTGACGCTGGCGGCCAGATGATCTGAATCAA 417
 Db 361 TCGGGTCCGCTCTACATGTTGACGCTGGCGGCCAGATGATCTGAATCAA 420
 Qy 418 AG-CTTTCTCTATACCTCTAGATGGAGCTGAGGAGATTGTCGGGTTG 475
 Db 421 AGTTTCTCTATACCTCTAGATGGAGCTGAGGAGATTGTCGGGTTG 480
 Db 421 AGTTTCTCTATACCTCTAGATGGAGCTGAGGAGATTGTCGGGTTG 480
 Qy 477 CTGGCTACTGGTAGGACTAATCGTAGATTGGTACACA 533
 Db 481 CTGGCTACTGGTAGGACTAATCGTAGATTGGTACACA 537
RESULT 9
 Locus S70398 545 bp RNA linear VRL 23-SBP-1994
 Definition [LTR, U3, R and U5 regions, long terminal repeats, provirus]
 Organism Reticuloendotheliosis virus
 Accession S70398
 Version S70398.1 GI:147134
 Keywords
 Source Reticuloendotheliosis virus
 Reference Viruses; Retroviridae; Gammaretrovirus.
 Authors Filardo,E.J., Lee,M.F. and Humphries,E.H.
 Title Structural genes, not the LTRs, are the primary determinants of reticuloendotheliosis virus A-induced runting and bursal atrophy
 Journal Virology 202 (1), 116-128 (1994)
 MEDLINE 9429132
 PUBLMED 800826
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 148190] from the original journal article.
 This sequence comes from Fig. 3.

FEATURES

source

1. .545 /organism="Reticuloendotheliosis virus"
 /mol_type="genomic RNA"
 /db_xref="taxon:11636"

ORIGIN

Query Match 82.3%; Score 438.4; DB 14; Length 545;
 Best Local Similarity 93.1%; Pred. No. 7.6e-124; Indels 26; Gaps 3;
 Matches 501; Conservative 0; Mismatches 11; db_xref="taxon:11636"

Qy 22 ATCTGGAGGAGCTCGGGGAATAGCGCTGCTACTGCATATTAGCTCT 81
 Db 1 AATGTGGAGGAGCTCGGGGAATAGCGCTGCTACTGCATATTAGCTCT 60
 Qy 82 GATATCATGCTCTCTGCTTACCGCCATTGACTGTGATATTCTCGTAT----- 134
 Db 61 GATATCATGCTCTCTGCTTACCGCCATTGACTGTGATATTCTCGTAT----- 120
 Qy 135 -----ATCATTTCTCGAAATGGCAATGGCTTAACCATAAAG 182
 Db 121 CTGGAAATCGGAACTTCTCGAAATGGCTTAACCATAAAG 180
 Qy 183 GAATGTTGTTGAGGAGGAGCTGAGGAACTTGACATGGTGAAGGGAGATCTCTCATGG 242
 Db 181 GAATGTTGTTGAGGAGGAGCTGAGGAACTTGACATGGTGAAGGGAGATCTCTCATGG 240
 Qy 243 AGATGAACTACATGAGGAACTTGACATGGCTTAACCATAAAG 302
 Db 241 AGATGAACTACATGAGGAACTTGACATGGCTTAACCATAAAG 300
 Qy 303 GAAAATGTCATGCACAC-----TCTGTAAGCGCTATAACCCAGGTGCACTCTGC 357
 Db 301 GAAAATGTCATGCACAC-----TCTGTAAGCGCTATAACCCAGGTGCACTCTGC 360
 Qy 358 TCAGGGTCCGCTCTACATGTTGACGCTGGCGCCAGATGATCTGAATCAA 417
 Db 358 TCAGGGTCCGCTCTACATGTTGACGCTGGCGCCAGATGATCTGAATCAA 417
 Db 359 GAAAATGTCATGCACAC-----TCTGTAAGCGCTATAACCCAGGTGCACTCTGC 360
 Qy 359 GAAAATGTCATGCACAC-----TCTGTAAGCGCTATAACCCAGGTGCACTCTGC 360

RESULT 10
 Locus S79845 583 bp DNA linear VRL 07-MAY-1993
 Definition [REV LTR] [Marek disease virus, attenuated strain JM-Hi3, reticuloendotheliosis virus insertion, Insertion, 583 nt].
 Organism Gallid herpesvirus 2
 Accession S79845
 Version S79845.1 GI:244514
 Keywords
 Source Gallid herpesvirus 2
 Reference 1 (bases 1 to 583)
 Authors Isfort,R., Jones,D., Kost,R., Witter,R. and Kung,H.J.
 Title Retrovirus insertion into herpesvirus in vitro and in vivo
 Journal Proc. Natl. Acad. Sci. U.S.A. 89 (3), 991-995 (1992)
 PubMed 9214243
 Remark GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 79845] from the original journal article.
 This sequence comes from Fig 1C.

FEATURES

source

1. .583 /organism="Gallid herpesvirus 2"
 /insertion_seq=""
 /mol_type="genomic DNA"
 /db_xref="taxon:10390"

ORIGIN

Query Match 80.5%; Score 429; DB 14; Length 583;
 Best Local Similarity 93.1%; Pred. No. 6.1e-121; Indels 26; Gaps 4;
 Matches 501; Conservative 0; Mismatches 11; db_xref="taxon:10390"

Qy 22 AATGTGGAGGAGCTCGGGGAATAGCGCTGCTACTGCATATTAGCTCT 81
 Db 563 AATGTGGAGGAGCTCGGGGAATAGCGCTGCTACTGCATATTAGCTCT 504
 Qy 82 GATATCATGCTCTCTGCTTACCGCCATTGACTGTGATATTCTCGTAT----- 134
 Db 503 GATATCATGCTCTCTGCTTACCGCCATTGACTGTGCTGCTGCTACTGCATATTAGCTCT 444
 Qy 135 -----ATCATTTCTCGAAATGGCTTAACCATAAAG 182
 Db 443 CTGGAAATCGGAACTTCTCGAAATGGCTTAACCATAAAG 180
 Qy 183 GAATGTTGTTGAGGAGGAGCTGAGGAACTTGACATGGCTTAACCATAAAG 242
 Db 333 GAATGTTGTTGAGGAGGAGCTGAGGAACTTGACATGGCTTAACCATAAAG 324
 Qy 243 AGATGAACTACATGAGGAACTTGACATGGCTTAACCATAAAG 302
 Db 323 AGATGAACTACATGAGGAACTTGACATGGCTTAACCATAAAG 264
 Qy 303 GAAAATGTCATGCACAC-----TCTGTAAGCGCTATAACCCAGGTGCACTCTGC 357
 Db 263 GAAAATGTCATGCACAC-----TCTGTAAGCGCTATAACCCAGGTGCACTCTGC 204
 Qy 358 TCAGGGTCCGCTCTACATGTTGACGCTGGCGCCAGATGATCTGAATCAA 417
 Db 358 TCAGGGTCCGCTCTACATGTTGACGCTGGCGCCAGATGATCTGAATCAA 417
 Db 359 GAAAATGTCATGCACAC-----TCTGTAAGCGCTATAACCCAGGTGCACTCTGC 360
 Qy 359 GAAAATGTCATGCACAC-----TCTGTAAGCGCTATAACCCAGGTGCACTCTGC 360

Query Match		38.7%	Score 206.4;	DB 14;	Length 1022;
		Best Local Similarity	99.1%;	Pred. No. 3.3e-52;	
		Matches	218;	Conservative	0;
		Mismatches	0;	Indels	1;
		Gaps	1;		
Db	398 AGATTCGAACTGTTAAGCTTCTCATATCCTCAGATGGCAGTGAGGAG 457				
Oy	459 AGATTCAATCGTAACTAA-CTTTTCTCTGAATCTCAGATGGCAGTGAGGAG 517				
Db	458 ATTTGTCGCTGCTGGCTGCCTACTGGGGGG-GTAGGATCCGGACTGATCGT 516				
Oy	518 ATTGTCGCTGCTGGCTGCCTACTGGGGGG-GTAGGATCCGGACTGATCGT 577				
Db	517 ACTTTCGGTACACA 533				
Oy	578 AGTACTTCGGTACACA 594				
Db	RESULT 13				
AF005066	AF005066 AF005066	1022 bp	DNA	linear	VRL 16-SEP-1997
LOCUS	POXVIRUS				
DEFINITION	Poxvirus S envelope glycoprotein (env) gene, partial cds and 3' long terminal repeat, complete sequence.				
REFERENCE	1 (bases 1 to 1022)				
AUTHORS	Hertig,C., Coupar,B.E., Gould,A.R. and Boyle,D.B.				
TITLE	Field and vaccine strains of cowpox virus carry integrated				
JOURNAL	Field and vaccine strains from the avian retroviruses, reticuloendotheliosis virus				
MEDLINE	Virology 235 (2), 367-376 (1997)				
PIBMED	9748585				
REFERENCE	2 (bases 1 to 1022)				
AUTHORS	Herrig,C.H., Coupar,B.E.H., Gould,A.R. and Boyle,D.B.				
TITLE	Direct Submission				
JOURNAL	Submitted (30-MAR-1997) Division of Animal Health, CSIRO, 5 Portarlington Road, Geelong, Victoria 3213, Australia				
FEATURES	Location/Qualifiers				
Source	1. 1022 /organism="Poxpox virus" /mol_type="genomic DNA" /strain="S (Standard Vaccine strain)"				
CDS	/db xref="taxon:10261"				
gene	/note="standard vaccine strain from Cyanamid-Webster PRY Ltd, Castle Hill, New South Wales, Australia integrated reticuloendotheliosis virus" <1..382> /gene="env"				
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</product="envelope glycoprotein"					
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/protein_id="AAC58241.1"					
/db_xref="GI:2393897"					
/translation="NRGLDILWTAACGGCIALQEKCPVANKSGIVRKIRKQDLDL					
LTR	IARKLYDPLWLNGFLPYLLPLGLPLFLPCISKLTIRIHAQSGSKNPSIQSPAVQVTPNPKDGYPRSMI" 409..679				
LTR	/note="3' LTR of reticuloendotheliosis provirus; LTR has deletions in U3, R, U5 regions; first 23 bp of U3 have been duplicated." 750..>1022				
CDS					
/notes="ORF1"					
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/protein_id="AAC58242.1"					
/db_xref="GI:2393898"					
/translation="MDITNTWTFDQPNIDNPINPYDIEKPLIVYSCDSYRLYNAK DNNPLSLKTFPCPSKNSRPIKEDILLRSIQSERVILKQYLDI"					
FEATURES	Location/Qualifiers				
Source	1. .495 /organism="Poxpox virus" /mol_type="genomic DNA" /strain="vaccine strain - Chick-n-pox"				
CDS	/db_xref="taxon:10261"				
	/note="From Fort Dodge Animal Health, Fort Dodge, IA identical sequence also found in strains FP-WAC (Intervet, Inc., Millsboro, DE), Poxpox (Mallinckrodt Veterinary, Inc., Millsboro, DE), Poxpox (Intercontinental Biologics, Millisboro, DE), Pigeonpox (Intervet, Inc., Millisboro, DE), vaccines for Poxvirus from Schering-Plough Animal Health, Omaha, NE and Select Laboratories, Gainesville, GA"				
	<1..60				
	/note="hypothetical protein; ORF1"				
	/codon_start=1				
	/evidence="not experimental"				
	/product="ORF2"				
	/protein_id="AAC21494.1"				
	/db_xref="GI:31267697"				
	/translation="KNDTSUPVAVKVIYGTVTI"				

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On nucleic - nucleic search, using SW model
Run on: May 25, 2004, 00:25:56 ; Search time 351 Seconds
(without alignments)
6450.967 Million cell updates/sec

Title: US-10-623-891-2
Perfect score: 533

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Identity_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409941 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001s:
5: geneseqn2001bs:
6: geneseqn2002s:
7: geneseqn2003bs:
8: geneseqn2003cs:
9: geneseqn2004s:
10: geneseqn2004s:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	506.8	95.1	512	AAX26109
2	506	94.9	536	AAX26110
3	506	94.9	4643	AAX26113
4	439.4	82.4	940	Aav6378
5	206.4	38.7	296	AAX26111
6	206.4	38.7	1022	AAX26115
7	193	36.2	298	AAX26112
8	193	36.2	1100	AAX26114
9	193	36.2	266145	ADE8477
10	155	29.1	578	Aav63779
11	145	27.2	3878	AQ76041
12	145	25.7	5528	AAQ76038
13	134.6	25.3	2	AQ76039
14	127.6	23.9	5519	AQ76040
C	15	33.8	6.3	714
C	16	33.8	6.3	4 AAK3652
C	17	33.8	6.3	2604 4 AAK94345
C	18	33.8	6.3	13079 5 ABA8638
C	19	33.8	6.3	25967 5 ABA8639
C	20	33.8	6.3	96960 7 ACP62734
C	21	33.8	6.3	96960 7 ADD20849
C	22	33.8	6.3	96960 9 ADB87938
C	23	33.8	6.3	96960 9 ADB96921

24	33.8	6.3	96960	9 ADB92112	Adb92112 Human MDR	
25	33.8	6.3	123785	7 ABX77171	Abx77171 DNA Sequ	
26	33.4	6.3	2000	7 ADA71938	Ada71938 Rice gene	
C	27	33.4	6.3	3824	9 ADE6320	Ad6320 Human gen
C	28	33.4	6.3	3824	9 ADE63196	Ad63196 Human gen
C	29	33.4	6.3	3824	9 ADE63208	Ad63208 Human can
C	30	33.4	6.3	3824	9 ADE63204	Ad63204 Human gen
C	31	33.4	6.3	6617	4 AA197964	Aai97964 Laweria
C	32	33.4	6.3	6617	8 ACB92322	Ac92322 Laweria
C	33	33.2	6.2	2000	7 ADAT1938	Ada71938 Rice gene
C	34	33	6.2	557	6 ABN61561	Abn61561 Human can
C	35	33	6.2	4703	3 AACT6621	Aac76621 Human can
C	36	33	6.2	11000	2 AAV21209_07	Continuation (8 of
C	37	32.6	6.1	96595	8 ADA02726	Ada02726 Human SYK
C	38	32.6	6.1	96595	9 ADB72464	Abd72464 Human SYK
C	39	32.2	6.0	703	4 AAK92046	Aak92046 Human CDN
C	40	32.2	6.0	703	4 AAK3694	Aak93694 Human CDN
C	41	32.2	6.0	3388	7 AAD47154	Ada47154 Human nuc
C	42	32.2	6.0	3396	4 AAK94808	Aak94808 Human full
C	43	32.2	6.0	3410	7 ABX10998	Abx70998 Novel hum
C	44	32.2	6.0	2046	8 ADB66951	Abd66951 E. coli K
C	45	32	6.0	9347	6 ABL49336	Ab49336 Human pol

CC when transfected into cell cultures and when chickens are infected. The present invention provides the means by which a FPV vaccine free from contamination by REV may be produced. (Updated on 17-OCT-2003 to standardise OS field)

XX

SQ Sequence 512 BP; 130 A; 113 C; 129 G; 140 T; 0 U; 0 Other;

Query Match

Best Local Similarity 95.1%; Score 506.8; DB 2; Length 512;

Matches 508; Conservative 99.6%; Pred. No. 8; 7e-162; Mismatches 2; Indels 0; Gaps 0;

QY

24 TGTGGAGGGAGCTCCGGGGAATAGCGCTGCTGCTACTGCATAATAGCTCTGT 83

1 TGTGGAGGGAGCTCCGGGGAATAGCGCTGCTGCTACTGCATAATAGCTCTGT 83

Db 84 AATCATGCTTGCCTTGCGCATGACTGATATTTGGCTGATATCATTCT 143

QY 61 AATCATGCTTGCCTTGCGCATGACTGATATTTGGCTGATATCATTCT 120

Db 144 CGAAATGGCATCAAGGAGCAAGCTCATAAACATAAAGGAATGTTGAGGAG 203

121 CGAAATGGCATCAAGGAGCAAGCTCATAAACATAAAGGAATGTTGAGGAG 203

Db 204 GTTACGCCATTCGACCATCATCACGAGAACACAGGAGATCGAACTACATCTGAG 263

QY 181 CATCATGACCAATTCGACCATCATCACGAGAACACAGGAGATCGAACTACATCTGAG 240

Db 264 CCAATGGTTGAAAGGCCAGATGCTATCCCTCAATGAGGAAATGTCAGCAATCT 323

QY 241 CCATGGTGTGAAAGGCCAGATGCTATCCCTCAATGAGGAAATGTCAGCAATCT 300

Db 324 GAAAGCGCTATAAGCCAGGTGATCTCTGCTGGGAGTCGGCTCTAACATTGT 383

301 GTAAACGGCTTATATGCCAGGTGATCTCTGCTGGGAGTCGGCTCTAACATTGT 360

QY 384 GTGACCTGCGGCCAGATTCATGATAAAGCTTTCCTATATCTCAGATT 443

361 GTGACCTGCGGCCAGATTCATGATAAAGCTTTCCTATATCTCAGATT 420

Db 444 CGCAGTGAGGAGATTTGTCGGGGCTGCGCTACTGGGTGGGGTAGGAATCC 503

QY 421 GGCACTGAGGAGGATTTGTCGGGGCTGCGCTACTGGGTGGGGTAGGAATCC 480

Db 504 504 GAGCTGAAATGGTAGTTGGTACACA 533

QY 481 GGACTGAAATGGTAGTTGGTACACA 510

RESULT 2
AAX26110

ID AAX26110 standard; DNA; 536 BP.

AC AAX26110;

XX DT 20-MAY-1999 (first entry)

DB Powpox virus (FPV M5) LTR sequence.

XX KW Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV; vaccine; chicken; LTR; long terminal repeat; ss.

XX OS Fowlpox virus.

XX WO9907852-A1.

XX PD 18-FEB-1999.
PF 07-AUG-1998; 98MO-AU000628.
XX PR 08-AUG-1997; 97AU-00008454.PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX

PI Hertig C, Coupar BEH, Gould AR, Boyle DB;
XX WPI; 1999-167428/14.

XX PT Recombinant vaccine against fowlpox virus - is free of contamination from
XX reticuloendotheliosis virus, used to prevent the virus occurrence in
PT chickens.

PS Claim 18; Fig 5; 127pp; English.

CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens older than 1 day can be vaccinated with the vaccine subsequent to vaccination with FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains of FPV carry integrated REV sequences. Some of the FPV strains carry a near full length provirus of REV, and can give rise to infectious REV. The present invention provides the means by which a FPV vaccine free from contamination by REV may be produced. Sequences AAX26110-115 represent FPV long terminal repeat sequences. The new recombinant FPV nucleic acid molecule can comprise a FPV LTR sequence selected from the above.

SQ Sequence 536 BP; 145 A; 115 C; 133 G; 143 T; 0 U; 0 Other;

Match 506; Conservative 100.0%; Pred. No. 1.7e-161; Mismatches 0; Indels 0; Gaps 0;

QY 28 GAGGGAGCTCCGGGGAGATAGCGCTGCTACTCCATTTACCTTCGTAATC 87

Db 89 ATCTCTGCTTCCTTACGCCATCTATCTGATATTTGCTATATCTCTGCA 148

QY 148 ATGGCATCAAGGAGGCTATAAACATAAAGGAATGTTGTTGAGGAGACATC 207

Db 149 ATGGCATCAAGGAGGCTATAAACATAAAGGAATGTTGTTGAGGAGACATC 208

QY 208 AGACCACTGACCACATCCAACTCACGAAACACAGGAGATGAACTATCTACTGAGCCA 267

Db 209 AGACCACTGACCACATCCAACTCACGAAACACAGGAGATGAACTATCTACTGAGCCA 268

QY 268 TGTGGTAAAGGGAGATGCTATCCCTCAATGGGAAATGTCATGCAACATCTGTA 327

Db 269 TGTGGTAAAGGGAGATGCTATCCCTCAATGGGAAATGTCATGCAACATCTGTA 328

QY 328 GGGCTATATAGCCAGGTGTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 387

Db 329 GGGCTATATAGCCAGGTGTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCA 388

QY 388 CGTGGGCCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 447

Db 389 CGTGGGCCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 448

QY 448 GTGAGGAGGATTTGTCGGGGCTACTGGGGGGGGGGGGGGGGGGGGGGGGGGGG 507

Db 449 GTGAGGAGGATTTGTCGGGGCTACTGGGGGGGGGGGGGGGGGGGGGGGGGG 508

QY 508 TGAATCCGTAGTATTCGGTACACA 533

Db 509 TGATCCGTAGTATTCGGTACACA 534

RESULT 3

AAX26113

ID AAX26113 standard; DNA; 4643 BP.

XX

FPV M (Cochin strain) acclimated with the vaccine subsequent to vaccination with FPV M (mild strain) at 1 day of age. Prior vaccine and field strains of FPV carry integrated REV sequences. Some of the FPV strains carry a near full length provirus of REV, and can give rise to infectious REV when transfected into cell cultures and when chickens are infected. The present invention provides the means by which a FPV vaccine free from contamination by REV may be produced. Sequences AAK6110-115 represent FPV long terminal repeat sequences. The new recombinant FPV nucleic acid molecule can comprise a FPV LTR sequence selected from the above

Query	Match	Score	DB	Length	Start	End	Similarity	Pred.	No.	Mismatches	Indels	Gaps	1;
Qy	1	38.7%	99.1%	3	206	2	DB 2;	Length	296;				
Matchers	218;	Conservative											
Db	1	TGTTGGAGGGAGCTCGGGGAATGTGGAGGGACCTCGGGGGGAATAGC5C7TGTCG	60	1	TGTTGGAGGGAGCTCGGGGAATGTGGAGGGACCTCGGGGGGAATAGC5C7TGTCG	60							
Db	1	TGTTGGAGGGAGCTCGGGGAATGTGGAGGGACCTCGGGGGGAATAGC5C7TGTCG	60	1	TGTTGGAGGGAGCTCGGGGAATGTGGAGGGACCTCGGGGGGAATAGC5C7TGTCG	60							
Qy	61	CTAACTCCATATTACTCTCGTAACTCATGCTGCTGCCTAGGCCCATGTGACTGTA	59	61	CTAACTCCATATTACTCTCGTAACTCATGCTGCTGCCTAGGCCCATGTGACTGTA	59							
Db	60	CTAACTCCATATTACTCTCGTAACTCATGCTGCTGCCTAGGCCCATGTGACTGTA	59	60	CTAACTCCATATTACTCTCGTAACTCATGCTGCTGCCTAGGCCCATGTGACTGTA	59							
Qy	121	TATATTCTGGTGTATCAATTCTCGGAATGGCATCGAGCATGAGCAGCTCATAACATAA	119	121	TATATTCTGGTGTATCAATTCTCGGAATGGCATCGAGCATGAGCAGCTCATAACATAA	119							
Db	120	TATATTCTGGTGTATCAATTCTCGGAATGGCATCGAGCATGAGCAGCTCATAACATAA	119	120	TATATTCTGGTGTATCAATTCTCGGAATGGCATCGAGCATGAGCAGCTCATAACATAA	119							
Qy	181	ACGAATGTTGTTGAGGAGGATCGACCACTTCAC	220	181	ACGAATGTTGTTGAGGAGGATCGACCACTTCAC	220							
Db	180	AGAAATGTTGTTGAGGAGGATCGACCACTTCAC	219	180	AGAAATGTTGTTGAGGAGGATCGACCACTTCAC	219							

ID AAX6115
 AAX6115 standard; DNA; 1022 BP.
 XX
 AC
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DB Fowlpox virus (FPV S) 3' LTR sequence.
 XX
 KW Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;
 KW vaccine; chicken; LTR; long terminal repeat; ss.
 XX
 OS Fowlpox virus.
 XX
 PN WO9907852-A1.
 XX
 PR 07-AUG-1998; 98WO-AU000628.
 XX
 PD 18-FEB-1999.
 XX
 PR 08-AUG-1997; 97AU-00008454.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PT Hertig C, Coupar BEH, Gould AR, Boyle DB;
 XX
 DR WPI; 1999-167428/14.
 XX
 PT Recombinant vaccine against fowlpox virus - is free of contamination
 CC reticuloendotheliosis virus, used to prevent the virus occurrence in
 CC chickens.
 XX
 PS Claim 18; Fig 6; 127pp; English.

CC vaccinated at older than 1 day of age. Alternatively, chickens older than
 CC 1 day can be vaccinated with the vaccine subsequent to vaccination with
 CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains
 CC of FPV carry integrated REV sequences. Some of the FPV strains carry a
 CC near full length proviruses of REV, and can give rise to infectious REV
 CC when transfected into cell cultures and when chickens are infected. The
 present invention provides the means by which a FPV vaccine free from
 CC contamination by REV may be produced. Sequences AAX2610-115 represent
 CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid
 CC molecule can comprise a FPV LTR sequence selected from the above
 XX

SQ Sequence 1022 BP; 315 A; 209 C; 218 G; 280 T; 0 U; 0 Other;

Query Match 38.7%; Score 206.4; DB 2; Length 1022;
 Best Local Similarity 99.1%; Pred. No. 5.9e-59; Mismatches 0; Indels 1; Gaps 1;
 Matches 218; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 TGTCGGAGGAGCTCGGGGAATGCGAGGAAGCTCGGGGCGAATAGCCTGGCTCG 60
 Db 409 TGTCGGAGGAGCTCGGGGAATGCGAGGAAGCTCGGGGCGAATAGCCTGGCTCG 467
 Qy 61 CTAACTGCATATTAGCTCTGTATCATGCCTCTGCCTACGCCATGTACTGA 120
 Db 468 CTAACTGCATATTAGCTCTGTATCATGCCTCTGCCTACGCCATGTACTGA 527
 Qy 121 TATATTGGCTGATATCATTTCTCGGAATCGCATAAGAGCAGGCTCATAAACCATAA 180
 Db 528 TATATTGGCTGATATCATTTCTCGGAATCGCATAAGAGCAGGCTCATAAACCATAA 587
 Qy 181 AGAAATGTTGTTGAGSCAACATCACACACTTGCA 220
 Db 588 AGAAATGTTGTTGAGSCAACATCACACACTTGCA 627

RESULT 7

AAX26112 Standard; DNA; 298 BP.

ID AAX26112;

AC AAX26112;

XX

DT 20-MAY-1999 (first entry)

XX

DB Fowlpox virus (FPV M3) LTR sequence.

KW Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV; vaccine; chicken; LTR; long terminal repeat; 88.

OS Fowlpox virus.

XX

PN WO9907852-A1.

XX

PD 18-FEB-1999.

PP 07-AUG-1998; 98WO-AU000628.

XX

PR 08-AUG-1997; 97AU-00008454.

XX

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX

PI Hertig C, Coupar BEH, Gould AR, Boyle DB;

XX

DR WPI; 1999-167428/14.

XX Recombinant vaccine against fowlpox virus - is free of contamination from
 PT reticuloendotheliosis virus, used to prevent the virus occurrence in
 PT chickens.

XX

PS Claim 18; FIG 5; 127pp; English.

CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic
 CC acid does not encode an active reticuloendotheliosis virus (REV), and
 CC whose genome does not contain any REV sequence. The recombinant FPV is
 CC used to produce a vaccine against fowlpox virus. The vaccine is used to

CC prevent the occurrence of fowlpox virus in chickens. The chickens can be
 CC vaccinated at older than 1 day of age. Alternatively, chickens older than
 CC 1 day can be vaccinated with the vaccine subsequent to vaccination with
 CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains
 CC of FPV carry integrated REV sequences. Some of the FPV strains carry a
 CC near full length proviruses of REV, and can give rise to infectious REV
 CC when transfected into cell cultures and when chickens are infected. The
 present invention provides the means by which a FPV vaccine free from
 CC contamination by REV may be produced. Sequences AAX2610-115 represent
 CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid
 CC molecule can comprise a FPV LTR sequence selected from the above
 XX

SQ Sequence 298 BP; 84 A; 59 C; 73 G; 82 T; 0 U; 0 Other;

Query Match 36.2%; Score 193; DB 2; Length 298;
 Best Local Similarity 100.0%; Pred. No. 5.5e-55; Mismatches 0; Indels 0; Gaps 0;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GGAGGAGACTCGGGGGATACGGCTGCTCTAATGCGCTATAGCTGCTGATAC 87
 Db 29 GGAGGAGACTCGGGGGATACGGCTGCTCTAATGCGCTATAGCTGCTGATAC 88
 Qy 88 ATGGTGTGCTTAGCGCCATGCGCTGTGATGATATTTGCGTGTATCATCTCGCA 147
 Db 89 ATGGTGTGCTTAGCGCCATGCGCTGTGATGATATTTGCGTGTATCATCTCGCA 148
 Qy 148 ATCGGCATCAAGCAGGCTCATAAACCATAAAGGAGATGTTGTTGAGGCAAGCTC 207
 Db 149 ATCGGCATCAAGCAGGCTCATAAACCATAAAGGAGATGTTGTTGAGGCAAGCTC 208
 Qy 208 AGACCACTGCA 220
 Db 209 AGACCACTGCA 221

RESULT 8

AAX26114 Standard; DNA; 1100 BP.

ID AAX26114;

AC AAX26114;

XX

DT 20-MAY-1999 (first entry)

XX

DB Fowlpox virus (FPV M3) LTR sequence.

KW Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV; vaccine; chicken; LTR; long terminal repeat; 88.

OS Fowlpox virus.

XX

PN WO9907852-A1.

XX

PD 18-FEB-1999.

PP 07-AUG-1998; 98WO-AU000628.

XX

PR 08-AUG-1997; 97AU-00008454.

XX

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX

PI Hertig C, Coupar BEH, Gould AR, Boyle DB;

XX

DR WPI; 1999-167428/14.

XX Recombinant vaccine against fowlpox virus - is free of contamination from
 PT reticuloendotheliosis virus, used to prevent the virus occurrence in
 PT chickens.

XX

PS Claim 18; FIG 6; 127pp; English.

CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic
 CC acid does not encode an active reticuloendotheliosis virus (REV), and
 CC whose genome does not contain any REV sequence. The recombinant FPV is
 CC used to produce a vaccine against fowlpox virus. The vaccine is used to

CC used to produce a vaccine against fowlpox virus. The vaccine is used to
 CC prevent the occurrence of fowlpox virus in chickens. The chickens can be
 CC vaccinated at older than 1 day of age. Alternatively, chickens older than
 CC 1 day can be vaccinated with the vaccine subsequent to vaccination with
 CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains
 CC near full length provirus of REV, and can give rise to infectious REV
 CC when transfected into cell cultures and when chickens are infected. The
 present invention provides the means by which a FPV vaccine free from
 CC contamination by REV may be produced. Sequences AAK26110-115 represent
 CC long terminal repeat sequences. The new recombinant FPV nucleic acid
 XX molecule can comprise a LTR sequence selected from the above

SQ

Sequence 1100 BP; 392 A; 177 C; 196 G; 335 T; 0 U; 0 Other;

Qy

Best Local Similarity

100.0%

Score

36.2%

DB

2

Length

1100

Matches

193

Conservative

0

Pred.

No.

1.1e-54

MisMatch

0

Indels

0

Gaps

0

Db

908

AGACCACTTGCAC

1100

Qy

208

ACACCACTTGCAC

220

Db

1088

AGACCACTTGCAC

1100

Qy

28

GGAGGGAGTCGCCAGGGGAATAGCGCTGCGTACTGCTAATAGCTCTGTAATC

87

Db

909

GGAGGGAGTCGCCAGGGGAATAGCGCTGCGTACTGCTAATAGCTCTGTAATC

967

Db

968

ATGCTTGCTTGCTTACGCCATTGACTGTGATATTGCGTGTATTCATTCTGGA

147

Db

1027

Qy

148

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207

Db

1028

ATCGGCACTAACAGCAGCTCTAACCCATTAAGGAATGTTGTTAACGAGATC

1087

Qy

209

ACACCACTTGCAC

220

Db

1088

AGACCACTTGCAC

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Qy

210

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147

Db

2211801

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221860

Qy

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207

Db

2211861

ATCGGCACTAACAGCAGCTCTAACCCATTAAGGAATGTTGTTAACGAGATC

221920

Qy

209

ACACCACTTGCAC

220

Db

221921

AGACCACTTGCAC

221933

Qy

210

GGAGGGAGTCGCCAGGGGAATAGCGCTGCGTACTGCTAATAGCTCTGTAATC

147

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2211801

ATGCTTGCTTGCTTACGCCATTGACTGTGATATTGCGTGTATTCATTCTGGA

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Qy

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221920

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209

ACACCACTTGCAC

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221921

AGACCACTTGCAC

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221860

Qy

149

ATCGGCACTAACAGCAGCTCTAACCCATTAAGGAATGTTGTTAACGAGATC

207

Db

2211861

ATCGGCACTAACAGCAGCTCTAACCCATTAAGGAATGTTGTTAACGAGATC

221920

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ACACCACTTGCAC

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Db

221921

AGACCACTTGCAC

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210

GGAGGGAGTCGCCAGGGGAATAGCGCTGCGTACTGCTAATAGCTCTGTAATC

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2211801

ATGCTTGCTTGCTTACGCCATTGACTGTGATATTGCGTGTATTCATTCTGGA

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210

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221860

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221921

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221933

Qy

210

GGAGGGAGTCGCCAGGGGAATAGCGCTGCGTACTGCTAATAGCTCTGTAATC

147

Db

2211801

ATGCTTGCTTGCTTACGCCATTGACTGTGATATTGCGTGTATTCATTCTGGA

221860

The universal retroviral vector pPO11-R1 (given in AAC076041) was obtained by replacing the SV40 promoter and hpt gene of pPO11-R1 (AAC076038) with the multiple cloning site of pBlueScript II KS. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes. (Updated on 25-MAR-2003 to correct PN field.)

XX	SQ	Sequence 3878 BP; 922 A; 948 C; 988 G; 1020 T; 0 U; 0 Other;
CC	Query Match	27.2%; Score 145; DB 2; Length 3878;
CC	Best Local Similarity	90.4%; Pred. No. 4.9e-38;
CC	Matches	189; Conservative 0; Mismatches 15; Indels 5; Gaps 3;
CC	QY	330 GGCTATATAAGCCAGGACATCTCTCTCGGGGTGGCTTCAACA---TTGTGTG 386
CC	Db	654 GTCTATATAGCAGAGCTCATCTCTCTCGGGTGGCTTCAACA 713
CC	QY	387 ACCTGCSCCCAGATGGAATGTAATAAA-GCTTTTCCTATATCTCAGATGG 445
CC	Db	714 ACCTGCSCCCAGATGGAATGTAATAAAACTT-TTTCATCTCAGATGG 773
CC	QY	446 CAGTGAGGAGGATTGTTCTGGGTGGCTACTGGGGG-GTAGGGTCCG 504
CC	Db	774 CAGTGAGGAGGATTGTTCTGGGTGGCTACTGGGGG-GTAGGGTCCG 833
CC	QY	505 GACTGAAATCGTAGTATTCTGGTACACA 533
CC	Db	834 GACTGAATCCGTTACTTCGGTACACA 862
XX	RESULT 12	
XX	ID AAQ76038 standard; DNA; 5528 BP.	
XX	AC AAQ76038;	
XX	DT 25-MAR-2003 (revised)	
XX	DT 20-JUL-1995 (first entry)	
XX	DE Retrovirus vector pPO11-R1.	
XX	KW Retrovirus; vector; pPO11-R1; spleen necrosis virus; SNV; cytomegalovirus; CMV; intermediate early promoter; IE promoter; long terminal repeat; LTR; encapsidation; gene transfer; gene therapy; SS.	
XX	OS Spleen necrosis virus.	
XX	PN WO9429437-A1.	
XX	PD 22-DEC-1994.	
XX	PR 07-JUN-1994; 94WO-US006415.	
XX	PR 07-JUN-1993; 93US-00073345.	
XX	PA (UNIV-) UNIV NEW JERSEY.	
XX	PI Dortenburg RC;	
XX	DR WPI; 1995-036467/05.	
PS	Example; Page 13-14; 28pp; English.	
XX	PT Recombinant retrovirus vector, conta. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect host cell and form provirus.	
XX	PT New recombination-free, highly efficient retroviral vectors pPO11-R1 (given in AAC076038), pPO11-R2 (AAC076039) and pPO11-R3 (AAC076040) were obtained by replacing the left region of the left LTR of spleen necrosis virus with the IE promoter/enhancer of CMV, and extension of the	

Matches	168;	Conservative	0;	Mismatches	9;	Indels	5;	Gaps	3;		
Qy	357	CCTGGGATGCCPCTACACA--TGTGTGAGTCAGCCGCGCAGATTCGATCTGAA	413	Qy	394	GCCAGATTCGAATCTGAAATAAGCTTTCTCTATCCAGATGGGAGTGA	453	Qy	394	GCCAGATTCGAATCTGAAATAAGCTTTCTCTATCCAGATGGGAGTGA	453
Db	672	CTCGGGGTCGCGRCCTGCACTATGTTGTTGAGTCAGCCGAGATTCGAA	731	Db	530	GTCMAAATCCCATCAGTCACAAAGCTTAATCTCTGATCAGCACGCTGCCTGAT	471	Db	530	GTCMAAATCCCATCAGTCACAAAGCTTAATCTCTGATCAGCACGCTGCCTGAT	471
Qy	414	TAATA-GCTTTCTCTATCCAGTTGGCAGTGAGGAGATTGTTGTTGGTG	472	Qy	454	GGAGATTGTTGGTTGTTGTTGCTGCTACTCTGGGTTGGGATCCGCTGATC	513	Qy	454	GGAGATTGTTGGTTGTTGTTGCTGCTACTCTGGGTTGGGATCCGCTGATC	513
Db	732	TAAACTTTTTCGAACTCAGTTGGAGGATTTGTTGTTGTTGTTGTTG	791	Db	470	TGAGATGTCCTCTGTTAGCTCTCAGGGCAGAGCTAGGGACAGGGC	411	Db	470	TGAGATGTCCTCTGTTAGCTCTCAGGGCAGAGCTAGGGACAGGGC	411
Qy	473	TCTGCTGACCTACTGGTGGG-CTAGGGATCCGACTGATCCGATGTTGTTG	531	Qy	514	CGTG 518		Qy	514	CGTG 518	
Db	792	TTCGCTGGCTACTGGTGGGCGCAGGGATCCGACTGATCCGATGTTGTTG	851	Db	410	CGAG 406		Db	410	CGAG 406	
Qy	532	CA 533									
Db	852	CA 853									

RESULT 15

AAK91988/C

ID AAK91988 standard; cDNA; 714 BP.

XX

AC AAK91988;

XX

DT 06-NOV-2001 (first entry)

XX

DB Human cDNA 5'-end sequence, SEQ ID NO: 448.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX

OS Homo sapiens.

XX

PN EF1130094-A2.

XX

PD 05-SEP-2001.

XX

PP 07-JUL-2000; 2000BP-00114089.

XX

PR 08-JUL-1999; 99JP-00194486.

XX

PR 11-JAN-2000; 2000JP-00118774.

XX

PR 02-MAY-2000; 2000JP-00183765.

XX

PA (HELI-) HELIX RES INST.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ora T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX DR WPI; 2001-524255/58.

XX

PT 830 Primers useful for synthesizing full length cDNA clones and their use

PT in genetic manipulation.

XX PS Claim 2; SEQ ID NO 448; 1380pp + Sequence Listing; English.

XX

The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' - and 3' - ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO

Sequence 714 BP; 136 A; 215 C; 193 G; 167 T; 0 U; 3 Other; SQ

Query Match Similarity 6.3%; Score 33.8; DB 4; Length 714;
Best Local Similarity 54.4%; Pred. No. 1.6;
Matches 68; Conservative 0.; Mismatches 57; Indels 0; Gaps 0;

Search completed: May 25, 2004, 02:15:46
Job time : 355 sec

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Om nucleic - nucleic search, using sw model

Run on: May 25, 2004, 01:24:46 ; Search time: 87 seconds
 (without alignments)
 3399.872 Million cell updates/sec

Title: US-10-623-891-2

Perfect score: 533

Scoring table: IDENTITY_NUC
 Gapp 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents No.:

- 1: /cgn2_6/podata/2/1na/5A_COMB.seq;*
- 2: /cgn2_6/podata/2/1na/5B_COMB.seq;*
- 3: /cgn2_6/podata/2/1na/6A_COMB.seq;*
- 4: /cgn2_6/podata/2/1na/6B_COMB.seq;*
- 5: /cgn2_6/podata/2/1na/PCTUS_COMB.seq;*
- 6: /cgn2_6/podata/2/1na/backfiles1.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
c 1	33.4	6.3	6617	Sequence 1, Appli
c 2	33	6.2	166496	Sequence 1, Appli
c 3	32	6.0	9347	Sequence 36, Appli
c 4	31.4	5.9	8878	Sequence 1, Appli
c 5	31.4	5.9	18609	Sequence 1, Appli
c 6	30.8	5.8	21110	Sequence 11, Appli
c 7	30.4	5.7	832	Sequence 2813, Appli
c 8	30.4	5.7	19233	Sequence 45, Appli
c 9	30.4	5.7	123005	Sequence 1, Appli
c 10	30.2	5.7	458	Sequence 77, Appli
c 11	30.2	5.7	458	Sequence 77, Appli
c 12	30.2	5.7	1071	Sequence 145, Appli
c 13	30	5.6	603	Sequence 5, Appli
c 14	30	5.6	603	Sequence 5, Appli
c 15	30	5.6	2907	Sequence 1, Appli
c 16	30	5.6	2907	Sequence 55, Appli
c 17	30	5.6	2907	Sequence 55, Appli
c 18	30	5.6	2907	Sequence 55, Appli
c 19	29.8	5.6	513	Sequence 348, Appli
c 20	29.8	5.6	513	Sequence 348, Appli
c 21	29.8	5.6	513	Sequence 348, Appli
c 22	29.8	5.6	513	Sequence 348, Appli
c 23	29.8	5.6	513	Sequence 348, Appli
c 24	29.8	5.6	4221	Sequence 22, Appli
c 25	29.8	5.6	4221	Sequence 22, Appli
c 26	29.8	5.6	5314	Sequence 15, Appli
c 27	29.8	5.6	41708	Sequence 3, Appli

ALIGNMENTS

RESULT 1
 US-09-689-065B-1/C

; Sequence 1, Application US/09689065B.
 ; Patent No. 6605696

; GENERAL INFORMATION:
 ; APPLICANT: PFILE Products, Inc.

; TITLE OF INVENTION: LAMSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND
 ; PILE REFERENCE: 3153_00187/PC1059A

; CURRENT APPLICATION NUMBER: US/09/689, 065B

; CURRENT FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: US Prov. 6/0160, 922

; PRIOR FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: US Prov. 6/0163, 858

; PRIOR FILING DATE: 1999-11-05

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 1

; LENGTH: 6617

; TYPE: DNA

; ORGANISM: Lawsonia intracellularis

; US-09-689-065B-1

Query Match 6.3%; Score 33.4; DB 4; Length 6617;
 Best Local Similarity 51.7%; Pred. No. 0.57; Mismatches 71; Indels 0; Gaps 0;

Matches 76; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Oy 226 ATTCAGCGACAAACAGGATGCAACTATCATGTGCCAACYGGTGTAAAGGCAGAT 285

Db 1775 AATGTAGGAGCTAAAGTCAACTCTATTAGCGTTCTGTGTAATAGGGAAAG 1716

Oy 286 GTATCCTCCAGTAGGGAATACTGCACTCACATCTGTAAGCGGTATATAAGCCAG 345

Db 1715 GATAACCTCTGCTGCTGGGTGCGCGTCC 1656

Oy 346 TGATCTCTGCTGCTGGCTGCTTC 372

Db 1655 ACCTCCCTGCTGCTGGCATTC 1629

RESULT 2
 US-08-916-421B-1

; Sequence 1, Application US/08916421B
 ; Patent No. 6503729

; GENERAL INFORMATION:
 ; APPLICANT: Built et al.

; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus jannaschii

; Patent No. 6503729

; TITLE OF INVENTION: jannaschii

; FILE REFERENCE: PB275

Sequence 11, Appli
 Sequence 5, Appli
 Sequence 3, Appli
 Sequence 3, Appli
 Sequence 3, Appli
 Sequence 17, Appli
 Sequence 17, Appli
 Sequence 17, Appli
 Sequence 3, Appli
 Sequence 8, Appli
 Sequence 11, Appli
 Sequence 12, Appli
 Sequence 34, Appli
 Sequence 2518, Appli

CURRENT APPLICATION NUMBER: US/08/916,421B
 CURRENT FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: US 60/024,428
 PRIORITY FILING DATE: 1996-08-22
 NUMBER OF SEQ ID NOS: 3
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 LENGTH: 1664976
 TYPE: DNA
 ORGANISM: Methanococcus jannaschii
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 OTHER INFORMATION: n equals a, t, c, or g
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 LOCATION: (84773)..(84773)
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 LOCATION: (559241)..(559241)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (600992)..(600992)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (622708)..(622708)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (657081)..(657081)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (682442)..(682442)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (674435)..(674435)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (682442)..(682442)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
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 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (741684)..(741684)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (779455)..(779455)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (779676)..(779676)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (855539)..(855539)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (871619)..(871619)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1087830)..(1087830)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1097846)..(1096846)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1119881)..(1119881)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1130881)..(1130881)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1132241)..(1132241)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (13109881)..(13109881)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (13132241)..(13132241)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1349473)..(1349473)
 OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc feature
; LOCATION: (1349491)..(1349491)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
; US-08-916-421B-1

Query Match
Best Local Similarity 6.2%; Score 33; DB 4; Length 1664976;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 177 TAAAGGAATGTTGTGAGGGAGCTCAGACACTTGACCATTACACGACA 236
Db 763297 TTAATAAATAATGCTCTACTTCACTCTCCATACATCAATAGC 763356
Qy 237 AACACGAGATGCACTATCATCTGAGCCATGGTGTAAAGGCAGATGCTTCCTCCA 296
Db 763357 CAGTAGATRACTCATATCATATTAACTTAATACAAACCTTATCTCTCCA 763416
Qy 297 A 297
Db 763417 A 763417

RESULT 3
US-10-204-708-36/C
Sequence 36, Application US/10204708
; Patent No. 667731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIRPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 1002529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 36
; LENGTH: 9347
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-204-708-36

Query Match 6.0%; Score 32; DB 4; Length 9347;

Best Local Similarity 48.4%; Pred. No. 2.2;
Matches 89; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy 137 CATTCTCGGAATGGCTCAAGAGCAGCTTAACATAAAGGAATGTTGTA 196
Db 1675 CAATTCCTCTTCCAAATACACAAACCTCAAAATGACCGATACGATACTA 1616
Qy 197 AGGCAAGGTCAGACACTTGACCATTACACGACAACAGGAGATGACTATCA 256
Db 1615 CGCTTATATCCGAGACTTAAACAAAGAAATCACAAATCACAAATCAAATAA 1556
Qy 257 TACTGAGCCAATGGTGTAAAGGCAGATGCTCAATCAGGGAAATGTCATCCA 316
Db 1555 AAACCATCTAACCAACCTAAATAAACCGATCTCTACTTAAATACAAATAACTAA 1496
Qy 317 ACAT 320
Db 1495 ACAT 1492

RESULT 4
US-08-206-176-3/C
Sequence 3, Application US/08206176
; Patent No. 5633940
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
; APPLICANT: Dalrymple, Michael A
; APPLICANT: Prunkard, Donna B
; APPLICANT: Foster, Donald C
; TITLE OF INVENTION: Production of Fibrinogen in Transgenic
; TITLE OR INVENTION: Animals
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; COMPUTER: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,176
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-648
; REFERENCE/DOCKET NUMBER: 93-15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8878 base pairs
; TYPE: nucleic acid
; STRANDBENDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE: CLONE: human fibrinogen B-beta chain
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 1..469
; FEATURE:
; NAME/KEY: exon
; LOCATION: 470..583
; FEATURE:
; NAME/KEY: intron
; LOCATION: 584..3257

FEATURE:
 NAME/KEY: exon
 LOCATION: 3258..3449
 FEATURE:
 NAME/KEY: intron
 LOCATION: 3450..3938
 FEATURE:
 NAME/KEY: exon
 LOCATION: 3939..4122
 FEATURE:
 NAME/KEY: intron
 LOCATION: 4123..5042
 FEATURE:
 NAME/KEY: exon
 LOCATION: 5043..5270
 FEATURE:
 NAME/KEY: intron
 LOCATION: 5271..5830
 FEATURE:
 NAME/KEY: exon
 LOCATION: 5831..5944
 FEATURE:
 NAME/KEY: intron
 LOCATION: 5945..6632
 FEATURE:
 NAME/KEY: exon
 LOCATION: 6633..6758
 FEATURE:
 NAME/KEY: intron
 LOCATION: 6759..6966
 FEATURE:
 NAME/KEY: exon
 LOCATION: 6967..7252
 FEATURE:
 NAME/KEY: intron
 LOCATION: 7253..7870
 FEATURE:
 NAME/KEY: exon
 LOCATION: 7871..8102
 FEATURE:
 NAME/KEY: 3' UTR
 LOCATION: 8103..8537
 FEATURE:
 NAME/KEY: misc_RNA
 LOCATION: 8538..8878
 FEATURE:
 NAME/KEY: CDS
 LOCATION: Join(470..583, 3258..3449, 3939..4122, 5043..5270,
 US-08-206-176-3)
 Query Match 5.9%; Score 31.4; DB 1; Length 8878;
 Best Local Similarity 57.7%; Pred. No. 3.5;
 Matches 56; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
 Qy 84 ATATCAGCTGCTGGCTTAGCGGCCATGTGATATTTCGCTGATCATCTCT 143
 Db 1109 AAAAAGCAATTCTTCACTACACTGATTTGATTTGCCTTGTAGCTAGT 1050
 Qy 144 CGGAATCGCCATCAGACGAGGTATAAACCTAA 180
 Db 1049 TATATTTTATAATAGTAATCTCAGTAACATA 1013
 RESULT 5
 US-08-943-731-1
 ; Sequence 1, Application US/08943731
 ; GENERAL INFORMATION:
 ; APPLICANT: PROKOP, DARWIN J.
 ; APPLICANT: SPOTILA, LORETTA D.
 ; APPLICANT: DELTS, CONSTANTINOS D.
 ; APPLICANT: SEREDA, LARISA

APPLICANT: LARSON, ANDREA W.
 APPLICANT: PACK, MICHAEL
 APPLICANT: COLIGE, ALAIN
 APPLICANT: EARLI, JAMES
 APPLICANT: KORKKO, JARMO
 APPLICANT: ALA-KOKKO, LEENA, et al.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
 TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
 NUMBER OF SEQUENCES: 666
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
 STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
 CITY: PHILADELPHIA
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-7066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/943-731
 FILING DATE: 03-OCT-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212,322
 FILING DATE: 14-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/803, 628
 FILING DATE: 03-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: DOYLE LEARY P.N.D., KATHRYN
 REGISTRATION NUMBER: 36,317
 REFERENCE/DOCKET NUMBER: 9598-27
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-965-1284
 TELEFAX: 215-567-2991
 TELEX: 831-49-49
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18609 base pairs
 STRANDEDNESS: single
 TYPE: nucleic acid
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-943-731-1
 Query Match 5.9%; Score 31.4; DB 3; Length 18609;
 Best Local Similarity 53.7%; Pred. No. 5.7;
 Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
 Qy 393 AGATCGGATCTGTAATAAACGACTTTCCTCTATATCCAGATGGCGTGAGAGGG 457
 Db 5286 AGGTAAGGGCTGTCGACATCATGGCTCCACATCCCAGAGCTCCACCATGATCA 5345
 Qy 458 ATTGTGTTGCTGCTGCTGCTGCTGCTACTGGCTGGGTAGGATCGGACTGATCCGA 517
 Db 5346 ATTCTGCTCATATCTCTGATCATACAGGTGACGCTGAGCTGAGATAGGA 5405
 Qy 518 G 518
 Db 5406 G 5406
 RESULT 6
 US-09-453-702B-111/c
 ; Sequence 11, Application US/09453702B
 ; Patent No. 6365723
 ; GENERAL INFORMATION:
 ; APPLICANT: Blattner, Frederick R.
 ; APPLICANT: Blattner, Valerie

Petra, Nicole T.
 Plunkett, Guy
 Welch, Rod

TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADRESSEER: Quarles & Brady
 STREET: 1 South Pinckney Street
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B
 FILING DATE: 03-Dec-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 6/0/110,955
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27386
 REFERENCE/DOCKET NUMBER: 960296..95017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-5000
 TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 111:

SEQUENCE CHARACTERISTICS:

LENGTH: 21119

MOLECULE TYPE: DNA (genomic)

STRANDBEADNESS: double

TOPOLOGY: linear

TYPE: nucleic acid

US-09-453-702B-111

Query Match 5.8%; Score 30.8; DB 4; Length 21119;
 Best Local Similarity 52.3%; Pred. No. 10; Mismatches 68; Conservatve 0; Indels 0; Gaps 0; Matches 28;

Qy 176 ATAAAGGAAATGGTTGTGAAAGCAAGCATGACACTTGCCACATCCATCAGCAC 235
 Db 12614 ATTATGCTTAAATTACATAGAACAGCCAAAAGTTAACAGTAATTAC 12555

Qy 236 AAACACGAGATCGAACTATCATACTGAGCCATGTTGAAGGGCAGATGTATCC 295
 Db 12554 AGTTGGTTGTAATGGCCAAATTTGAAAGGGTGTACAATCCCGAT 12495

Qy 296 AATGAGGAA 305
 Db 12494 CATGCTGAA 12485

RESULT 7
 US-09-621-976-2813

Sequence 2813, Application US/09621976

PATENT NO. 6633063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

; SEQ ID NO 2813

RESULT 8
 US-10-204-708-45/C

Sequence 45, Application US/10204708

PATENT NO. 667731

GENERAL INFORMATION:

APPLICANT: OLER, Alexander

APPLICANT: PIRENROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

PRIOR APPLICATION NUMBER: PCT/EP01/03971

PRIOR FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 45

LENGTH: 19233

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

FEATURE: NAME/KEY: unsure

LOCATION: (76, 178..179, 273, 585, 648, 651, 920, 1014, 1173, 1197, 1228)

OTHER INFORMATION: n is a or g or c or t

FEATURE: NAME/KEY: unsure

LOCATION: (1264, 1267, 1559, 1607, 1677, 1703, 1742, 1848, 1850, 2033)

OTHER INFORMATION: n is a or g or c or t

FEATURE: NAME/KEY: unsure

LOCATION: (2168, 2254, 2257, 2280, 2291, 2723, 3018, 3080, 4205, 4209)
 OTHER INFORMATION: n is a or g or c or t
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (4216, 4225, 4239, 4246, 4254, 4265, 4270, 4274, 4288, 4294, 4295)
 OTHER INFORMATION: n is a or g or c or t
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (4787, 4825, 4829, 4938, 4855, 5462, 5494, 5496, 5500, 5674)
 OTHER INFORMATION: n is a or g or c or t
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (4928, 4363, 4610, 4627, 4675, 4693, 4698, 4738, 4777, 4781)
 OTHER INFORMATION: n is a or g or c or t
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (5690, 5697, 5705, 5715, 5890, 5910, 5913, 6027, 6080, 6109)
 OTHER INFORMATION: n is a or g or c or t
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (6059, 8075, 8632, 8636, 9700, 9717, 9815, 9818, 9867, 9879)
 OTHER INFORMATION: n is a or g or c or t
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (6244, 6288, 6776, 6873, 6891, 6980, 7028, 7656, 7876, 8030)
 OTHER INFORMATION: n is a or g or c or t
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (6805, 1075, 10150, 10159, 10165, 10356, 11123, 11166, 11360)
 OTHER INFORMATION: n is a or g or c or t
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (11703, 11933, 12050, 12340, 12981, 13564, 13764..13765, 13787)
 OTHER INFORMATION: n is a or g or c or t
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (13846, 14168, 15565, 17006, 17217, 17650, 17653, 17656, 1798)
 OTHER INFORMATION: n is a or g or c or t
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (18130, 18143, 18151, 18188, 18498, 18549, 18936, 18946, 19165)
 OTHER INFORMATION: n is a or g or c or t
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (19300)
 OTHER INFORMATION: n is a or g or c or t
 0-204-708-45
 LT 9
 9-198-452A-1
 quence 1, Application US/09198452A
 tent No. 655294
 INTERNAL INFORMATION:
 PPLICANT: Griffais, R.
 TITLE OF INVENTION: chlamydia pneumoniae genomic sequence and polypeptides, fragments
 TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
 DENT REFERENCE: 9710-003-999
 CURRENT APPLICATION NUMBER: US/09/198,452A
 CURRENT FILING DATE: 1998-11-24
 NUMBER OF SEQ ID NOS: 6849
 SEQ ID NO 1
 LENGTH: 1230025
 TYPE: DNA
 ORGANISM: Chlamydia pneumoniae
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(1500)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
 LOCATION: (1501)..(3000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
 LOCATION: (3001)..(4500)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
 LOCATION: (4501)..(6000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
 LOCATION: (6001)..(7500)
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 LOCATION: (7501)..(9000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
 LOCATION: (9001)..(10500)
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 NAME/KEY: misc_feature
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 NAME/KEY: misc_feature
 LOCATION: (18001)..(19500)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
 LOCATION: (195001)..(210000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
 LOCATION: (210001)..(225000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
 LOCATION: (225001)..(240000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
 LOCATION: (240001)..(255000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
 LOCATION: (255001)..(300000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
 LOCATION: (300001)..(315000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature
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 OTHER INFORMATION: n=a or c or g or t

LOCATION: (330001)..(345000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (345001)..(360000)
 OTHER INFORMATION: n=a or c or g or t
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 OTHER INFORMATION: n=a or c or g or t
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 LOCATION: (420001)..(435000)
 OTHER INFORMATION: n=a or c or g or t
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 OTHER INFORMATION: n=a or c or g or t
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 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (510001)..(525000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (525001)..(540000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (540001)..(555000)
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 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (585001)..(600000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (600001)..(615000)
 OTHER INFORMATION: n=a or c or g or t
 LOCATION: (615001)..(630000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (630001)..(645000)
 OTHER INFORMATION: n=a or c or g or t
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 LOCATION: (645001)..(660000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (660001)..(675000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (675001)..(690000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (690001)..(705000)

OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (705001)..(720000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (720001)..(735000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (735001)..(750000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (750001)..(765000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (765001)..(780000)
 OTHER INFORMATION: n=a or c or g or t
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 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (795001)..(810000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (810001)..(825000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (825001)..(840000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (840001)..(855000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (855001)..(870000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (870001)..(885000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (885001)..(900000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (900001)..(915000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature

Query Match 5.7%; Score 30.4; DB 4; Length 1230025;
 Best Local Similarity 54.5%; Pred. No. 1.5e+03; Matches 61; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 17 GGGGAATGTGGAGGGGCTCGGGGGAAATAGCGCTGGCTACTGCATATTAG 76
 Db 638954 GGAAATGATATCTCATGATTCAGGAGATGGCTTACCCATATGGATCAATAAG 639013

QY 77 CTCTGTTATCAGTCCTTGCTTGCCTAGGCCATTCTACTGATATPTTC 128
 Db 639014 CTTCATCTCTCTTTTCCATATGATGAGCTATGAGCTATTTC 639065

RESULT 10
 US-09-221-228-77/c
 Sequence 77, Application US/9921298
 Patent No. 6284241
 GENERAL INFORMATION:
 APPLICANT: XU Jianguchun
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
 FILE REFERENCE: 210121_471
 CURRENT APPLICATION NUMBER: US/09/221,298
 CURRENT FILING DATE: 1998-12-23
 NUMBER OF SEQ ID NOS: 112
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 77
 LENGTH: 458

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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (196)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE: modified_base
; NAME/KEY: modified_base
; LOCATION: (409)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE: modified_base
; NAME/KEY: modified_base
; LOCATION: (410)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE: modified_base
; NAME/KEY: modified_base
; LOCATION: (417)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE: modified_base
; NAME/KEY: modified_base
; LOCATION: (442)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE: modified_base
; NAME/KEY: modified_base
; LOCATION: (447)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE: modified_base
; NAME/KEY: modified_base
; LOCATION: (450)
; OTHER INFORMATION: Where n is a, c, g or t
; OTHER INFORMATION: Where n is a, c, g or t
; US-09-221-298-77

Query Match      5.7%; Score 30.2; DB 3; Length 458;
Best Local Similarity 53.4%; Pred. No. 1.4;
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
Qy   376 ACATCTGGGACGCGGCCAGATCGAACTGTAAATAAGCTTTCTCTATAC 435
Db   287 ACATATTGGGATGATGAGTATGGATGTTCAAAGCTTTCTCTATTC 228
Qy   436 CTCAGATGGGAGGAGGATTTGTCGGTGTGGCTACTGGTG 491
Db   227 CTCATATGAGGAATGAGGGCATACATTGGTAGGGTGTCTGGTG 172

RESULT 11
US-09-401-064-77/C
Sequence 77, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
; APPLICANT: Charles Kunisch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; OPERATING SYSTEM: MSDOS Version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brooke, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB440P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-145

Query Match      5.7%; Score 30.2; DB 4; Length 10711;
Best Local Similarity 48.5%; Pred. No. 11; Matches 112; Conservative 0; Mismatches 118; Indels 1; Gaps 1;
Qy   210 ACCACTGGCACCATCCATCAGAACAAAGAGATCGAACTTCATACTGGCCATG 269
Db   5925 ACCAATTGCAAGTAAGTGTGATACCACTTCAGACGACATTCAGAGTAC 5866
Qy   270 GTGTAAGGGAGATGCTTCAATGGGAATTCATCGAACATCTGTAAG 329
Db   5865 ATTGAGACGTCGCTCAAGTGTAAAGAAGGCTACAGTTGGAGTACTGTC 5806
Qy   330 GCTATATACCCAGGTGCACTCTGCTGGGTRGCCCTCACACATGTTGACG 389
SEQ ID NO 77
LENGTH: 458
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:

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RESULT 13
US-08-816-346-5
; Sequence 5, Application US/08816346
; Patient No. 6127525
GENERAL INFORMATION:
; APPLICANT: Crystal, Ronald G.
; APPLICANT: Falck-Pedersen, Erik
; APPLICANT: Koveedi, Imre
; APPLICANT: Wickham, Thomas J.
TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND
TITLE OF INVENTION: METHODS OF USING SAME
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
; STREET: TWO PRUDENTIAL PLAZA - 4900
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,346
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 67167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/616-5600
; TELEFAX: 312/616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 603 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-816-346-5
Query Match 5.6%; Score 30; DB 3; Length 603;
Best Local Similarity 55.9%; Pred. No. 2;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
Query 97 TGCCCTTACGCCGCAATTGACTGTATATTTCGCGATTCGGAAATCGGCATC 156
Db 410 TGCCTCTTCCAAGGTGACTTGCAATTCTCAATACTACCTCTTGACGACCGC 469
Query 157 AAGGAGCAGGCTATAACCATATAAGGAATGTTGTAAG 198
Db 470 AACGCAATGCTACTAAACCAAAGTGTGTTGACAGTGAG 511
; US-08-816-346-5
RESULT 15
US-08-816-346-1
; Sequence 1, Application US/08816346
; Patient No. 6127525
GENERAL INFORMATION:
; APPLICANT: Crystal, Ronald G.
; APPLICANT: Falck-Pedersen, Erik
; APPLICANT: Gall, Jason
; APPLICANT: Koveedi, Imre
; APPLICANT: Wickham, Thomas J.
TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND
TITLE OF INVENTION: METHODS OF USING SAME
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
; STREET: TWO PRUDENTIAL PLAZA - 4900
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,346
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 67167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/616-5600
TELEFAX: 312/616-5700
TELEX: 25-353
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2907 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match 5.6%; Score 30; DB 3; Length 2907;
Best Local Similarity 55.9%; Pred. No. 5.5;
Matches 57; Conservancy 0; Mismatches 45; Indels 0; Gaps 0;
Qy 97 TGCCTTAGCCCATGTACTTGATATTCGATATCATTCCTCGAATGGCAGC 156
Db 803 TGCCTCTCAAGGTGACTTGCAATCTCTCAATACCTACCTCTTGAAACCGC 862
Qy 157 AAGAGCAGGCTATAACATAAGGAATGTTGTTGAG 198
Db 863 AAGGCATGCTRACTAACCAAAGTGGTTGACAGTGAG 904

Search completed: May 25, 2004, 02:59:18
Job time : 92 secs

GenCore version 5.1.6
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On nucleic - nucleic search, using BW model
 Run on: May 25, 2004, 01:32:27.; Search time 339 Seconds
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Title: US-10-623-891-2
 Perfect score: 533

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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2953838 seqs, 2272363821 residues
 Total number of hits satisfying chosen parameters: 5907676

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : Published Applications NA.*

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19: /cgn2_6/ptodata/1/pubpna/us60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	ALIGNMENTS
C 1	35	6.6	328	13	US-10-142-426-34	Sequence 34, App1
C 2	35	6.6	328	15	US-10-123-155-34	Sequence 34, App1
C 3	35	6.6	328	15	US-10-146-731-34	Sequence 34, App1
C 4	35	6.6	328	15	US-10-140-472-34	Sequence 34, App1
C 5	35	6.6	328	15	US-10-141-761-34	Sequence 34, App1
C 6	35	6.6	328	15	US-10-142-885-34	Sequence 34, App1
C 7	35	6.6	328	15	US-10-158-790-34	Sequence 34, App1
C 8	35	6.6	328	16	US-10-137-871-34	Sequence 34, App1
C 9	35	6.6	328	16	US-10-140-923-34	Sequence 34, App1
C 10	35	6.6	328	16	US-10-141-567-34	Sequence 34, App1
C 11	35	6.6	328	16	US-10-141-759-34	Sequence 34, App1
C 12	35	6.6	328	16	US-10-140-805-34	Sequence 34, App1
C 13	35	6.6	328	16	US-10-140-864-34	Sequence 34, App1
C 14	34	6.4	616	13	US-10-142-426-206	Sequence 205, App

Best local Similarity 6.9%; Pred. No. 0.67; Length 328;

Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCATGCTACTTGATATTGCTGATCATTCCTGGAAATCGCCATCAAGA 160
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN...B.Y.NHSKS...S..N.S..Y.SDK. 263

QY 161 GCAGGCTCATAACATAACGAAATGTTGTGAAGGCAAGCATCAGACCACTTGAC 220
Db 262 KYA.RB.MNK..WSTA.RG..AKSCHRA..SSA..R...N.C..RTHNRA.YA.AH 203

QY 221 CATCCAATCAGAACACAGAGATGCACTATCATGCAATGGCTTAAAGGG 280
Db 202 YN.KYN..NSSHSBM..SBBB.CN.SMTT.ABNAR..DNRD..B.CS.T.CN..D.S 143

QY 281 CAGATGCTATCCTCCAACTGAGGAAATGTCATGCACATCTGTAGGCCATATAAG 340
Db 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANKRACSBMCCAN.Y..A 83

QY 341 CCAGGTGATCTTGCCTGGGGTCTGGCTTACACATGTTGACGTCGGCCAGA 400
Db 82 ..H..KDSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWNC.D.M.SN. 23

QY 401 TTC 403
Db 22 .TS 20

RESULT 2
US-10-123-155-34/c
; Sequence 34, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanaabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C23
; CURRENT APPLICATION NUMBER: US/10/146,731
; CURRENT FILING DATE: 2005-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PR
; ORGANISM: Homo Sapien
; US-10-146-731-34

Query Match 6.6%; Score 35; DB 15; Length 328;
Best Local Similarity 6.9%; Pred. No. 0.67;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCATGCTACTTGATATTGCTGATCATTCCTGGAAATCGCCATCAAGA 160
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN...B.Y.NHSKS...S..N.S..Y.SDK. 263

QY 161 GCAGGCTCATAACATAACGAAATGTTGTGAAGGCAAGCATCAGACCACTTGAC 220
Db 262 KYA.RB.MNK..WSTA.RG..AKSCHRA..SSA..R...N.C..RTHNRA.YA.AH 203

QY 221 CATCCAATCAGAACACAGAGATGCACTATCATGCAATGGCTTAAAGGG 280
Db 202 YN.KYN..NSSHSBM..SBBB.CN.SMTT.ABNAR..DNRD..B.CS.T.CN..D.S 143

QY 281 CAGATGCTATCCTCCAACTGAGGAAATGTCATGCACATCTGTAGGCCATATAAG 340
Db 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANKRACSBMCCAN.Y..A 83

RESULT 4
US-10-140-472-34/c
Publication No. US/10140472
GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Thomas, Daniel K.
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Yau, Ah
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 FILE REFERENCE: P3330R1C168
 CURRENT APPLICATION NUMBER: US/10/140,472
 CURRENT FILING DATE: 2002-05-06
 PRIOR APPLICATION removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 550
 LENGTH: 328
 TYPE: PRT
 ORGANISM: Homo sapien
 SEQ ID NO 34
 LENGTH: 328
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-141-701-34

Query Match 6.6%; Score 35; DB 15; Length 328;
 Best Local Similarity 6.9%; Pred. No. 0.67; Indels 0; Gaps 0;
 Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCCATGCTACTGTGATATTTCGGATATCGGCATCGAACATCGAAGA 160
 DB 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN...B.Y.NHSKS...S.N.S.Y.SDK. 263
 QY 161 GCGGGCTCATAAACCATAAAGGAATGTTGTGAAGGCAACCATGAGCAACTTGAC 220
 DB 262 KVA.RB.MNK..WSTA.RG..AKSCHRA..SSA..R...N.C..RTHNRA.YA.AH 203
 QY 221 CATTCAAATCACGACAAACACAGAGATGCAACTATCAGCCAACTCTGTAAAGGG 280
 DB 202 YN.KYN...NSSHSBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN.D.S 143
 QY 281 CAGATGCTATCCCTCAATGAGGAATGTCATGCAACATCTGTAAAGGGTATAAG 340
 DB 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANKRACSBMYCAY..A 83
 QY 341 CCAGGTGATCTCTGCTCGGGCTGCCACATGTGTGAGCTGGGGCCAGA 400
 DB 82 ..H..KDSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWNC.D.M.SN. 23
 QY 401 TEC 403
 DB 22 .TS 20

RESULT 5
US-10-141-701-34/c
Sequence 34, Application US/10141761
Publication No. US20030148432A1
GENERAL INFORMATION:
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Thomas, Daniel K
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 FILE REFERENCE: P3330R1C168
 CURRENT APPLICATION NUMBER: US/10/141,761
 CURRENT FILING DATE: 2002-05-08
 Prior Application removed - See Palm or File Wrapper
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 34
 LENGTH: 328
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-141-701-34

Query Match 6.6%; Score 35; DB 15; Length 328;
 Best Local Similarity 6.9%; Pred. No. 0.67; Indels 0; Gaps 0;
 Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCCATGCTACTGTGATATTTCGGATATCGGCATCGAACATCGAAGA 160
 DB 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN...B.Y.NHSKS...S.N.S.Y.SDK. 263
 QY 161 GCGGGCTCATAAACCATAAAGGAATGTTGTGAAGGCAACCATGAGCAACTTGAC 220
 DB 262 KVA.RB.MNK..WSTA.RG..AKSCHRA..SSA..R...N.C..RTHNRA.YA.AH 203
 QY 221 CATTCAAATCACGACAAACACAGAGATGCAACTATCAGCCAACTCTGTAAAGGG 280
 DB 202 YN.KYN...NSSHSBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN.D.S 143
 QY 281 CAGATGCTATCCCTCAATGAGGAATGTCATGCAACATCTGTAAAGGGTATAAG 340
 DB 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANKRACSBMYCAY..A 83
 QY 341 CCAGGTGATCTCTGCTCGGGCTGCCACATGTGTGAGCTGGGGCCAGA 400
 DB 82 ..H..KDSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWNC.D.M.SN. 23
 QY 401 TEC 403
 DB 22 .TS 20

RESULT 6
US-10-142-885-34/c
Sequence 34, Application US/10142885
Publication No. US20030157604A1
GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc

RESULT 7
US-10-158-790-34/c
; Sequence 34, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C448
CURRENT APPLICATION NUMBER: US/10/158,790
CURRENT FILING DATE: 2002-05-30
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-142-885-34
Query Match 6.6%; Score 35; DB 15; Length 328;
Best Local Similarity 6.9%; Pred. No. 0.67; Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;
QY 101 TTAGCCGCCATTGACTTGATATTCGGATATCGGAATCTCGAAATCGCATCAAGA 160
Db 322 BYR..M.TYNN.GHMC..S.N.NAV.GYNN...B.Y.NHSKS...S.N.S.Y.SDK. 263
QY 161 GCAGGCCTCATATAAACATAAAGGAATGTTGTGAAGGCAACATGACACTTGAC 220
Db 262 KVA.RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C..RTHNRA.YA.AH 203
QY 221 CATCCAACTCACACACACACAGAGATGCAACTATCACTGAGCCATGTAAAGG 280
Db 202 YN.KYN..NSSHSBM..SBBB.CN.SMTT.ABNR..DNRD...B.CS.T.CN.D.S 143
QY 281 CAGATGTTATCCTCCATAGGGAAATGTCATGCAACATCTGTAGCGCTATAAG 340
Db 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANKACSBMYCCAN.Y.A 83
QY 341 CCAGGTCATCTGTCGGGTCCCGTCTACATGTCAGCTGACCTGGCCAGA 400
Db 82 ..H..KDSA..NB.S.YMCBSG.NWTISNB.CW.S.B.B.SC.BB.MRTWC.D.M.SN. 23
QY 401 TTC 403
Db 22 .TS 20
RESULT 8
US-10-137-871-34/c
; Sequence 34, Application US/10137871
; Publication No. US20030207350A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Goddard, Paul J.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C153
CURRENT APPLICATION NUMBER: US/10/137,871
CURRENT FILING DATE: 2002-05-03

Prior Application removed - See Palm or File Wrapper
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 34
 LENGTH: 328
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-137-871-34

Query Match Best Local Similarity 6.6%; Score 35; DB 16; Length 328;
 Best Local Similarity 6.6%; Pred. No. 0.67; Mismatches 184; Indels 0; Gaps 0;
 Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCATGACTGTGATATTCTGGATCATTCCTCGGAATCGGCATCAGA 160
 DB 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN...B.Y.NHSKS...S.N.S..Y.SDK. 263

QY 161 GCAGGCTCATTAACCATAAAGGAATGTTGTTGAAGGCCAAGCATCGACACTTGAC 220
 DB 262 KYA.RB.MNK..WSTA.RG...AKSCHRA..SSA.R...N.C...RTHNMRA.YA.AH 203

QY 221 CATCGCAATTGACAAACAGAGATCGACTATCATCTGACGCCAATGTTGAAGGG 280
 DB 202 YN.KCN..NSSHSBM..SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN.D.S 143

QY 281 CAGATGCTATCCTCOAATGAGGAAATGTCATCGAACATCTGTAAGGGCTATATAG 340
 DB 142 C.SH.SC.D.Y...YDSBAK.CCS.NB.D.MH.Y.SDYCNRKACSBMYCCAN.Y.A 83

QY 341 CCAGGTGCATCTCTGCTGGGGTGGCCCTCTCACATGTTGTCGACGTGCGGCCAGA 400
 DB 82 ..H..KOSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWWC.D.M.SN. 23

QY 401 TTC 403
 DB 22 .TS 20

RESULT 9
 Sequence 34, Application US/10140923
 Publication No. US20030207355A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeBorge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Deyo, Paul J.
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritten, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hwang, Zemin
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: P3330RIC200

CURRENT APPLICATION NUMBER: US/10/141-756

CURRENT FILING DATE: 2002-05-08

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 34
 LENGTH: 328
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-141-756-34

Query Match Best Local Similarity 6.6%; Score 35; DB 16; Length 328;
 Best Local Similarity 6.6%; Pred. No. 0.67; Mismatches 184; Indels 0; Gaps 0;
 Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCATGACTGTGATATTCTGGATCATTCCTCGGAATCGGCATCAGA 160
 DB 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN...B.Y.NHSKS...S.N.S..Y.SDK. 263

QY 161 GCAGGCTCATTAACCATAAAGGAATGTTGTTGAAGGCCAAGCATCGACACTTGAC 220

RESULT 13
US-10-140-864-34/c
Sequence 34, Application US/10140864
Publication No. US20030207419A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Dennoyers, Luc
; APPLICANT: Gurney, Austin L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanae, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330RIC184
CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-864-34

Query Match 6.6%; Score 35; DB 16; Length 328;
Best Local Similarity 6.9%; Pred. No. 0; Gaps 0;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTACCGCCATGTTACTGTATATTTCGCTGATTCATTCTGGAAATCGGCATCAAGA 160
Db 322 BYR..M.TTN..GHNC...S.N.NAV.GYNN...B.Y.NHSK...S.N.S.Y.SDK. 263
QY 161 GCACGCTCATAACCTAAAGAGAATGTTTGTAGGCCAGCAGCACTTGAC 220
Db 262 KYA.RB.MNK..WSTA.RG...AKSCHRA..SSA.R...N.C...RTHNRA.YA.AH 203
QY 221 CATCCATCAGAACAGAGATCGAACATTAATCTACTGAGCCATAGGGTGAAGGG 280
Db 202 YN.KVN..NSSHSM..SBBB.CN.SMTR.ABNAR..DNRD..B.CS.T.CN.D.S 143
QY 281 CAGATGCTATCTCTCAAATGAGGAAATATGTCATGACATCCTGTAGCGCTATAATAG 340
Db 142 C.SH.SC.D.Y...YDSRKA.CCS.NB.D.MH.Y.SBDYCNKRACSBMVKCCAN.Y..A 83
QY 341 CCAGGGCATCTCTGCTCGGGTGGCCGCTACACATGTTGACGCGCGGCCAGA 400
Db 82 ...H..KDSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWNC.D.M.SN. 23
QY 401 TTC 403
Db 22 .TS 20

RESULT 14
US-10-142-426-206
; Sequence 206, Application US/10142426
; Publication No. US2004004333A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Dennoyers, Luc
; APPLICANT: Gurney, Austin L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanae, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330RIC224
CURRENT APPLICATION NUMBER: US/10/142,426
CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 206
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-426-206

Query Match 6.4%; Score 34; DB 13; Length 616;
Best Local Similarity 9.6%; Pred. No. 2.1; Mismatches 46; Conservative 124; Mismatches 308; Indels 0; Gaps 0; Gaps 0;

QY 18 GGGAAATGGGAGGGCTCCGGGGGATAGGGCTGCTGCTGACTGCCATATTAGC 77
Db 8 RESVRFRGTTYPALPSKNGKKWEILNFQYFEACKRAAKNSLIKGLERPHVGVLGFNSAE 67

QY 78 TTCTGTAAATCTCTGCTGCTGCTGCTTAGGCCCTAGTACTGTATATTTCGCTGATATC 137
Db 68 WFTPAVGAALLAGGLCVGVIYATNSABACOVTITHAKVNLIVENDOQLKLISIPOSSLR 127

QY 138 ATTCTCGGATCGCATCAAGACAGGCTCATTAACCATAAAGGAATGTTGTTGAA 197
Db 128 KALIIQYULPKMKNNLWSDDFMBLGSPIDPQEOLVIESOKANOCATLYITSGTTGIP 187

QY 198 GGCAAGCATAGACCACCTGACCATCCATCAGAACAAACAGAGATCGACATCAT 257
Db 188 KGVMILSHDNITWLAGAVTKDFKLTDKHETVNSTPLSHIAQMDIWPIKALITYFAQ 247

QY 258 ACTGAGCCATGTTGTAAGGCCAGAGGCTATCCTCCATAGGGAAAATGTCATGCA 317
Db 248 ADALKGLTVSLTEKVKEPVTFIGVPOIWERKHEMVKNLSKMGFLKKKAFKFWARNIGFKN 307

QY 318 CATCTGTAGCGCTATATAAGCCAGGTGATCTCTTCCTCGGGTCCCCGCTCTACAC 377
Db 308 SKOMLGKNTPSYRMKTLVSKUKTSILGDICHSPISGTAPLNQETAFFLSDLPIG 367

QY 378 ATTTGTGCTGAGCGGGGCCAGATTCGATCTGTTAATAAAAGCTTTCTCTMATCCT 437
Db 368 ELYGLSESSSGPHTISQNQYRLLSCGKLTGCKXNLFOONKDGEICLWGRHIFMGYLE 427

QY 438 CAGATTGCCAGTCAGAGGAGATTGTTGCTGCTGCTGCTACTCGGTGGGT 495
Db 428 SETETTEAIDBEGWLHSGDLDGLGLFLYVTSKHLITTAGENVPPVPIPVETLUK 485

Search completed: May 25, 2004, 03:05:08
Job time : 341 secs

GenCore version 5.1.6
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Om nucleic - nucleic search, using BW model
Run on: May 25, 2004, 01:20:42 ; Search time 2498 Seconds
(without alignments)
6371.714 Million cell updates/sec

Title: US-10-623-891-2
perfect score: 533
Sequence: 1 tggggaggagctccgggg.....cgtagtttcggtaacaaca 533

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqB, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : EST:
1: em_estba: *
2: em_estium: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpol: *
7: em_estio: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_e813: *
13: gb_e84: *
14: gb_e85: *
15: em_estun: *
16: em_estom: *
17: em_gse_hum: *
18: em_gse_inv: *
19: em_gse_pln: *
20: em_gse_vrt: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rnd: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_g802: *
29: gb_g802: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	39.4	7.4	1201	9 AL549619	AL549619 AL549619
2	38.2	7.2	621	28 BR767965	BR767965 BR767965
3	37.8	7.1	654	12 BI870967	BI870967 603395724
4	37.4	7.0	1265	10 BR128543	BR128543 601810690

COMMENT

Genoscope - Centre National de sequencage

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8081.r. For more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/clusterv.cgi?seq=CS0D1055AB070&cluster=8081.r>. Contact :

ALIGNMENTS

RESULT 1
AL549619
LOCUS AL549619 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA DEFINITION clone CS0D1055Y113 5'-PRIME, mRNA sequence.
ACCESSION AL549619
VERSION AL549619.2 GI:31271437
KEYWORDS EST,
SOURCE Homo sapiens (human),
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE I (bases 1 to 1201)
AUTHORS Li, W.B.; Gruber, C.; Jesse, J. and Polavie, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12885780.
Contact: Genoscope
Genoscope - Centre National de sequencage
BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/clusterv.cgi?seq=CS0D1055AB070&cluster=8081.r>. Contact :
Feng Liang Email : fliang@lifetech.com URL : <http://www.genoscope.cns.fr/cgi-bin/clusterv.cgi?seq=CS0D1055AB070&cluster=8081.r>

<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0bp055AB07QPI.

FEATURES source

- . . 1201
 - /organism="Homo sapiens"
 - /mol_type="mRNA"
 - /ab_xref="Taxon:9606"
 - /clone="CS0bp055Y13"
 - /tissue_type="PLACENTA COT 25-NORMALIZED"
 - /clone.Lib="Homo Sapiens PLACENTA COT 25-NORMALIZED"
 - /note="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 7.4%; Score 39.4; DB 9; Length 1201; Best Local Similarity 41.3%; Pred. No. 0; 83; Mismatches 81; Indels 0; Gaps 0; Matches 74; Conservative

QY 145 GAACTGGCCTACAGAGCAGCTATAACCATAAAGGAAATCTTGTGAAGGCAGCA 205 Db 1022 GAAGCTGGYWRCTAAAGGAWCCAGGTAGTGTTGCGWTGTTAACGTTGAGAARAKATA 1081

QY 206 TCAAGGACTTGACCATCCATCACGACAACAGGAGTCGAACTTCAACTGAGGCC 265 Db 1082 AGAAWCCACTTGTCGTCASAYAWMTGAGCWCAGGAGATSGACYCWTGTTARMTTM 1141

QY 266 ATATGGTTGAAAGGCAGATGCTATCCCTCAATGAGGAAATGCTAGCAACATCTG 324 Db 1142 HGGGGGRGAIRGGGTMRAAMKSCAGGCCYCAARGGWWAAAACCTTKKCaGAGCCG 1200

RESULT 2

BH767965/c LOCUS BH767965 621 bp DNA linear GSS 20-MAR-2002 DEFINITION BMBAC372H04T7_PSU Brugia malayi Genomic Bac Library 3 Brugia malayi GENOMIC, genomic survey sequence.

ACCESSION BH767965.1 VERSION GI:19565729

KEYWORDS SOURCE

ORGANISM Brugia malayi

REFERENCE 1 (bases 1 to 621)

AUTHORS Whitten,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster,J., Guilliano,D., Slatko,B. and Blaxter,M.

TITLE Genome survey sequences from the human parasitic nematode Brugia malayi.

JOURNAL Unpublished (2000)

COMMENT Contact: Blaxter ML, Institute of Cell, Animal and Population Biology University of Edinburgh Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JT, UK Tel: +44 131 650 6760 Fax: +44 131 670 5450 Email: mark.blaxter@ed.ac.uk

Sequenced from the Brugia malayi BAC library constructed by Claire Whitten and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Edinburgh, UK. Seq primer: "T7" (TAATACGACTCACTATAGGG) Class: BAC ends.

FEATURES source

- 1. . 621
 - /organism="Brugia malayi"
 - /mol_type="genomic DNA"
 - /strain="TRS"
 - /db_xref="taxon:6279"
 - /sex="Mixed (male and female)"

ORIGIN

Query Match 7.2%; Score 38.2; DB 28; Length 621; Best Local Similarity 52.1%; Pred. No. 1; 5; Mismatches 78; Indels 0; Gaps 0; Matches 85; Conservative

QY 117 TGTGATATTGCGTGTGATCATTCATTCTCGGATCGCATCAAGAGCAGCAGCTCATTAACCA 176 Db 171 TAGATATTTAGGCGATTAATTCGGTCAAATCTTATTAATGTTAAGTGTATGGA 112

QY 177 TAAAGGAAATGTTGTTGAAGGCAAGCTAGACCCACTGCACCATCCATCAGGACA 236 Db 111 AATATATAAATTTCTTAAGAACATATTAAACAAAGAACATTAACAAAGGAACATTAATGCTG 52

QY 237 AACAGGAGATGAACTTCAACTGAGCCATGGTTGTAAGG 279 Db 51 ATCACTGAAATGATGTTAGCCGTAGTAATGAATGTTGATGG 9

RESULT 3

BB870967 LOCUS BI870967 654 bp mRNA linear EST 11-OCT-2001 DEFINITION 6039574F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5405813 5'

ACCESSION BI870967

VERSION 1.1. GI:16044640

KEYWORDS SOURCE

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 654)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NIH_MGC http://mgc.nci.nih.gov/.

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

TISSUE Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: <http://image.llnl.gov>

Plate: LUM12034 row: P column: 06

High quality sequence stop: 510.

FEATURES source

- 1. . 654
 - /organism="Homo sapiens"
 - /mol_type="mRNA"
 - /ab_xref="Taxon:9606"
 - /clone="IMAGE:5405813"
 - /tissue_type="adecarcinoma cell line"
 - /lab_host=DHL0B (phage-resistant)
 - /clone.Lib="NIH_MGC_90"
 - /note="Organ: liver vector: pCMV-SPORT6; site 1: NotI; Site 2: SalI; Cloned unidirectionally; Oligo-dT Primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
 - Note: this is a NIH_MGC library."

ORIGIN

Query Match 7.1%; Score 37.8; DB 12; Length 654;

Best Local Similarity 51.5%; Pred. No. 2:1;
Matches 87; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 85 ATCGTGTGCTTCCTTGCCGCATGTACTGATATTGGCTGATATCATTCTC 144
Db 461 ATTACTCTGTTACACTATGTTGTTAACATAATTATCATT 520

Qy 145 GGNATCGGCATCAAGAGCAGGCTCATAAACCTAAAGGAAATGTTGTGAGGCCAGC 204
Db 521 TTTCGGACTCAAGAAGAAACAAACAAACAAACAAAGAAATAAAAGAACACA 580

Qy 205 ATCAGACCCTGACCATCCAACTCACGACAAACAGAGATGCACTA 253
Db 581 AGGAAACATAACAAACAGAGAAAGAGAGAGAGAGATCGAACGA 629

RESULT 4
BF128543/c
LOCUS BF128543 1265 bp mRNA linear EST 24-OCT-2000
DEFINITION 6018106901 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053479 3', mRNA sequence.
ACCESSION BF128543
VERSION BF128543.1 GI:10967583
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1265)
AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgpsb@mail.nih.gov
Tissue Procurement: ARCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at:
http://image.llnl.gov
Plate: LILN892 row: d column: 24
High quality sequence start: 25
High quality sequence stop: 124.

FEATURES
source

FEATURES
source

ORIGIN

Query Match 6.9%; Score 37; DB 29; Length 745;
Best Local Similarity 53.0%; Pred. No. 4; Mismatches 79; Conservative 0; Indels 0; Gaps 0;

Qy 49 AGGCCTGCTCGTAACGCCATTACCTCTGTAATCAGTCGCTGCCTAGCCG 108
Db 164 AGGCCTGCTCGTAACGCCATTACCTCTGTAATCAGTCGCTGCCTAGCCG 223

Qy 109 CATTGCTATGATATTGCGTATACATCTCTCGCATCGCATAGAGCAGGCTC 168
Db 224 GTTATTAGATATTAGTTAATATAGTTGATTCGATTCGATGGAAAGAG 283

Qy 159 ATAAACCTTAANGGAATGTTGTA 197
Db 284 TCCCTCGAGAGAAACAGTTTTGA 312

RESULT 6
BFX81961/c
LOCUS BX81961 1201 bp mRNA linear EST 08-MAY-2003
DEFINITION BX81961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS01072YF05 3'-PRIME, mRNA sequence.
ACCESSION BX81961
VERSION BX81961.1 GI:30453007
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polaves,D.
TITLE Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91064 Evry Cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr

ORIGIN

Query Match 7.0%; Score 37.4; DB 10; Length 1265;
Best Local Similarity 58.6%; Pred. No. 3:7; Mismatches 65; Conservative 0; Indels 0; Gaps 0;
Matches 46; **Qy** 343 AGGTGCACTCTCTCTGGGGTCCCGCTTACCATGTTGTTACGAGCGGCCAGAT 402
Db 836 AGGGGGTTGAGCTCTCTGGGGTAGACATATTAGTGGCCACCTGTGTA 777
Qy 403 CGAATCTGTTAAAGCTTTCTATATCCTCAGATTGCGACTGAGA 453

COMMENT	- Web : www.genoscope.cns.fr/ Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org
FEATURES SOURCE	<p>melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammober in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library, or and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.</p>
FEATURES SOURCE	<p>1 . 999 'organism="Drosophila melanogaster" 'mol_type="genomic DNA" '/db_xref="taxon:7227" '/clone="BACR35P15" '/clone_l1b="RPCI-98" '/note="end : T7"</p>
ORIGIN	<p>Query Match 6.8%; Score 36.4; DB 29; Length 999; Best Local Similarity 41.4%; Pred. No. 7; Mismatches 77; Indels 0; Gaps 0;</p> <p>Matches 70; Conservative 22; Mismatches 77; Indels 0; Gaps 0;</p> <p>Qy 219 ACCATCCAACTCAGAACAGGATGCACATCATACTGACCAATGTTGAAG 278 Db 996 ASKGGAGGAAAGAACAAWWHWAATTAATGGGAAAGTGTGCAACATCCCTGTAAGGGCTATA 937 Qy 279 GCAGATGTCATTCCTCAAATGAGGAAATGTCATGCAACATCCCTGTAAGGGCTATA 338 Db 936 TGCTTAAMTWGGTCCCAAGKGKMCACWAAATGGYCTCCYCTTCCATTACCGGCCAMA 877 Qy 339 AGCGAGGTGCTCTTGCGCGGGTGCCTGTGTGTA 387 Db 876 WGGCATTTACGCCATTTCCTTAATTTCAGCAGAAGGGTGA 828</p>
RESULT 9	<p>AL525502/c AL525502 1201 bp mRNA linear EST 23-MAY-2003 DEFINITION Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo Sapiens ACCESSION AL525502 VERSION AL525502.2 KEYWORDS EST. SOURCE ORGANISM Homo sapiens (human)</p>
REFERENCE	<p>1 (bases 1 to 1201) Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wilie, T., Underwood, K., Steptoe, M., Theisinger, B., Allen, M., Bowers, Y., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.</p>
AUTHORS	<p>Li, W.B., Gruber, C., Jesse, J. and Polayes, D.</p>
TITLE	<p>Full-length cDNA libraries and normalization</p>
JOURNAL	<p>Unpublished (2001)</p>
COMMENT	<p>On Feb 13, 2001 this sequence version replaced gi:1278895.</p>
REFERENCE	<p>Contact: Genoscope Genoscope - Centre National de Séquençage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr/cgi-bin/clustter.cgi?seq=CS0DC012AG02NP1&cluster=2889.f. Contact : Feng Liang Email : fliang@lifeTech.com URL : http://fulllength.invitrogen.com Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DC012AG0NP1.</p>
FEATURES	<p>Location/Qualifiers Location/Qualifiers</p>
source	<p>1 . 1201 'organism="Homo sapiens" 'mol_type="mRNA" '/db_xref="taxon:9606" '/clone="CS0DC012M03" '/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED" '/clone_l1b="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED" '/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized." Organism Query Match 6.7%; Score 35.8; DB 9; Length 1201; Best Local Similarity 37.6%; Pred. No. 12; Mismatches 50; Indels 0; Gaps 0; Matches 50; Conservative 32; Mismatches 51; Indels 0; Gaps 0;</p> <p>Qy 117 TTGATATTTCTGATATCATTTCTGGAAATGGCTCAAGAGCAGCTCATAAACCA 176 Db 1154 TTAAWAWTTWTGARTWARTWTTSSVARPGWAATKTSRKRSTVAAAAG 1095 Qy 177 TAAGGAAATGTTGAGGAGGATCACACTTGACCATCANTCAGCAGCA 236 Db 1094 ATATAADATGTRKTWTGATGTYKAAGGAAAGTGTTTTAWWWAHARASMAATT 1035 Qy 237 AACAGGAGATCGA 249 Db 1034 WKTACAAATATG 1022</p> <p>RESULT 10 BI350586 BI350586 456 bp mRNA linear EST 26-JUL-2002 LOCUS BI350586 DEFINITION <i>fr3n04.yd</i> zebrafish adult brain Danio rerio cDNA clone IMAGE:4953825, mRNA sequence.</p> <p>ACCESSION BI350586 VERSION BI350586.1 GI:15045032 EST. SOURCE ORGANISM Danio rerio (zebrafish)</p> <p>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. Other ESTs: Fr33h04_x1 1 (bases 1 to 456) Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wilie, T., Underwood, K., Steptoe, M., Theisinger, B., Allen, M., Bowers, Y., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.</p> <p>WashU Zebrafish EST Project 1998 Unpublished (1998) Other ESTs: Fr33h04_x1 Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: zebrafishwton.wustl.edu</p> <p>CDNA Library Preparation: John Ngai, CDNA Library Arrayed by: Matthew Clark, DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.regenex.com) (email contact: info@regenex.com) and Ressourcenzentrumprimärdatenbank, Berlin, Germany (web address: www.rpd.de) Seq primer: T7 Location/Qualifiers 1 . 456 'organism="Danio rerio" 'mol_type="mRNA" '/db_xref="taxon:7955"</p>

/clone="IMAGE:4953382"
 /sex="mixed male and female"
 /tissue type="brain"
 /dev stage="adult"
 /lab_hob="E. coli DH10B"

/note="vector: pZPLOX; Site_1: NotI; Site_2: SalI;
 Original library was constructed in Lambda-ZPLOX. Mass
 excision of the cDNA library was performed to yield
 pZPLOX plasmids. Insert check was done in original

ORIGIN

Query Match Similarity 6.6%; Score 35.4; DB 12; length 456;
 Best Local Similarity 52.3%; Pred. No. 11; Mismatches 78;保守型 0; Indels 0; Gaps 0;
 Matches 78; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 49 AGGGCTGGCGCCTACTGCCTATTAGCTCTGTAATCATGCTGCTTGCCCTAGCCG 108
 Db 308 AGGGCTGGCTTCTTAGTATATAGAATGCTTGTCTGCCAGATCTCCAGGAGG 367

Qy 109 CATTGACTGATATATTGGCTGATATCAATTCTCGGAATGGCATCAAAGCAGGCTC 168
 Db 368 GTTTATTAGTATTATTTAGTCATAATAGTTGGAAATCTGTCATGGANAGAAG 427

Qy 169 ATAAACCTAAAGGAATGTTGTGAA 197
 Db 428 TTCTTCAGAAGAGAACCGTTTIGA 456

RESULT 11

BIJ308473

LOCUS BIJ308473 EST52983 GPOD Medicago truncatula mRNA clone pgPOD-TAIL 5, end,
 DEFINITION mRNA sequence.

ACCESSION BIJ308473

VERSION BIJ308473.1

KEYWORDS EST.

ORGANISM Medicago truncatula (barrel medic)

REFERENCE AUTHORS

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicots; rosids; euroids; Fabales; Fabaceae; Papilionoideae; Faboideae; Medicago.

1 (bases 1 to 339)

Grubak,M.A., Samac,D.A., Town,C.D., Van Aken,S., Utterback,T.,

Cho,J. and Fraser,C.M.

ESTs from developing reproductive tissues of Medicago truncatula

Unpublished (2001)

COMMENT Contact: Michael A. Grubak

Baylor College of Medicine

1100 Bates Street, Houston, TX 77030-2600, USA

Tel: 713-798-7044

Fax: 713-798-7078

Email: m.grubak@bcm.edu

TIGR sequence name: MT09006TK

More information is available at: www.medicago.org.

Seq primer: Kmrod (CMA GAA CTA gtg GAT CC).

Location/Qualifiers

FEATURES source

1 .339

/organism="Medicago truncatula"

/mol_type="mRNA"

/cull_val="All"

/db_xref="Taxon:3880"

/clone="pgPOD-TAIL"

/tissue_type="immature pod walls"

/dev_stage="Immature pods, ranging in age from 15 to 30 days after pollination"

/clone_id="GPOD"

/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:

XbaI; Immature pods, ranging in age From 15 to 30 days

ORIGIN

Query Match Similarity 6.6%; Score 35.2; DB 12; Length 339;
 Best Local Similarity 57.1%; Pred. No. 11; Mismatches 105;保守型 0; Indels 73; Gaps 6; Gaps 2;

Matches 105; Conservative 0; Mismatches 73; Indels 6; Gaps 2;

Qy 34 AGCCCGGGGATAGGCCAGCTGCCTACTGCATATTAGCTCTCTATCATGCT 93
 Db 48 ACCGCCGGGGATCCACCCCTGCTCTCCCTCGAGATCTGTATCAT 106Qy 94 GCTGCCTAGGCCATGTACTGATATT-----CGCTATATATTCTGGA 148
 Db 107 GACTCCGATCAGMATGACTGATGATGTTGTCGACCTGAAATCATGCTGAT 166Qy 149 TCGCATCAAGGAGGCCATAAACCATAAAGGAATGTTGTCGAGGCAATCA 208
 Db 167 TCTGTATGAGCATCATGAGAAATGAAATGATCATGATTCCATCARGA 226Qy 209 GACC 212
 Db 227 GAAC 230

RESULT 12

BH567971

LOCUS BH567971 BH567971 BOCH Brassica oleracea genomic clone BOCHG05, genomic

DEFINITION SURVEY Sequence.

VERSION BH567971

KEYWORDS GSS.

ORGANISM SOURCE

Brassica oleracea

REFERENCE AUTHORS

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicots; rosids; euroids; II; Brassicaceae; Brassica.

1 (bases 1 to 595)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.

TITLE Unpublished (2001)

COMMENT OTHER_GSS: BOCHG05TR

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Fax: 301-838-3523

Email: cdw@netgr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF Class: sheared ends.

FEATURES source

1 .595

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="Nol100DH3"

/db_xref="Taxon:712"

/clone="BOGH05"

/clone_id="BOGH05"

/notes="Vector: pRSI; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pRSI using BstXI linkers." after pollination, were collected from greenhouse-grown plants. At harvest, seeds were removed from pods and isolated pod walls were collected and immediately frozen in liquid nitrogen. Pod walls were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the UniZap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-assist helper phage and propagated in XL10R cells."

COMMENT

- Web : www.genoscope.cns.fr/
 Determination of this BAC-end sequence was carried out as part of a collaboration with the BDGP.

The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP *Drosophila melanogaster* BAC library was prepared by Kazuroyo Osegawa and Aaron Mammsoer in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RCGI-98 and was constructed by partial RccRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES source

Location/Qualifiers
 1. . 962
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BAC24H08"
 /clone_lib="RPCI-98"
 /note="end : TET3"

ORIGIN

Query Match 6.6%; Score 35.2; DB 29; Length 962;
 Best Local Similarity 27.7%; Pred. No. 17; Matches 46; Conservative 52; Mismatches 68; Indels 0; Gaps 0;
 Db 943 TATWCAKGKRTKRMMTKGKTTWTTAGKTTIANGKRAKAGAAMAWAHYRR 884
 Qy 162 CAGGCTCATTAACCTAAAGGAATGTGTGTCAGGAAAGCATCAGGCCATTGCACC 221
 Db 883 MASKITCMWTAMMMWWAWATGMCYTKKKNNWWAMAACTATGTMARYVAATKGKCMW 824
 Qy 222 ATCCAAATCAGGAAACACAGGAGTCGAACATCATCTGGCAA 267
 Db 823 AKRAAAGSWDRNTATWMCCDCCKKTAARMAWWWAATDGAVCAA 778

Search completed: May 25, 2004, 02:57:39
 Job time : 3504 secs